

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:01:55 ; Search time 90.0757 Seconds
(without alignments)
2239.886 Million cell updates/sec

Title: US-09-503-089A-5
Perfect score: 2042
Sequence: 1 MKQNVRLALIVCTFYLL.....STGLHSLSTFGLMKRRSV 394

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2042	100.0	394	1 CIW3 HUMAN	O14649 homo sapien
2	1850.5	90.6	411	1 CIW3_RAT	O54912 rattus norv
3	1840.5	90.1	409	1 CIW3_MOUSE	O35111 mus musculus
4	1732	84.8	392	2 Q9ESM5	RA Q9ESM5 rattus norv
5	1333	65.3	299	2 Q9QX34	RA Q9QX34 mus musculus
6	1298.5	63.6	301	2 Q9ESM4	RA Q9ESM4 rattus norv
7	1150	56.3	374	2 Q63Z10	Q63Z10 xenopus lae
8	1116	54.7	374	1 CIW9 HUMAN	Q9NPC2 homo sapien
9	1069.5	52.4	365	1 CIW9_CAVPO	Q9J158 cavia porce
10	999	48.9	396	2 Q923V6	Q923V6 rattus norv
11	960.5	47.0	395	2 Q9JLD4	Q9JLD4 rattus norv
12	924	45.2	237	1 CIW9_RAT	Q9ES08 rattus norv
13	916.5	44.9	318	1 CIW9_RAT	Q9H427 rattus norv
14	846	41.4	330	1 CIW9_HUMAN	Q9H427 homo sapien
15	820	40.2	329	2 O17185	RL O17185 caenorhabdi
16	777	38.1	340	2 Q9VHE0	Q9VHE0 drosophila
17	769	37.7	307	2 Q7PZH9	Q7PZH9 anopheles g
18	760.5	37.2	345	2 Q7QC61	Q7QC61 anopheles g
19	742	36.3	398	2 Q9VFS9	Q9VFS9 drosophila
20	732.5	35.9	370	2 Q9JL57	Q9JL57 cavia porce
21	599	29.3	364	2 Q76790	Q76790 caenorhabdi
22	558.5	27.4	121	2 Q867A3	Q867A3 oryctolagus
23	373	18.3	405	1 CIW2_MOUSE	Q8R1P5 mus musculus
24	370	18.1	411	1 CIW2_MOUSE	P97438 mus musculus
25	369	18.1	405	1 CIW2_RAT	Q9ES08 rattus norv
26	367	18.0	426	2 Q920B6	Q920B6 rattus norv
27	366	17.9	414	2 Q6P6P9	Q6P6P9 mus musculus
28	364	17.8	426	1 CIW2_HUMAN	Q95069 homo sapien
29	363	17.8	411	2 Q9NRT2	Q9NRT2 homo sapien
30	361	17.7	309	1 CIW9_HUMAN	Q9ET55 homo sapien
31	360	17.6	411	2 Q8HY88	Q8HY88 bos taurus

32	358.5	17.6	331	2 Q8AIV5	Q8AIV5 xenopus lae
33	358	17.5	408	1 CIW2_HUMAN	Q9H414 homo sapien
34	354	17.3	294	2 Q6X6Z5	Q6X6Z5 homo sapien
35	349.5	17.1	453	2 Q8BZB0	Q8BZB0 m mus muscu
36	349.5	17.1	535	2 Q8BUW1	Q8BUW1 m mus muscu
37	349.5	17.1	538	1 CIWA_HUMAN	P57789 homo sapien
38	349.5	17.1	538	1 CIWA_RAT	Q9J184 rattus norv
39	349.5	17.1	538	2 Q6Q834	Q6Q834 oryctolagus
40	349.5	17.1	543	2 Q6B014	Q6B014 homo sapien
41	346.5	17.0	262	2 Q6X6Z3	Q6X6Z3 homo sapien
42	345.5	16.9	426	2 Q8I6M6	Q8I6M6 aplysia cal
43	341	16.7	323	2 Q6PEI1	Q6PEI1 brachydanio
44	334.5	16.4	322	2 Q6X6Z4	Q6X6Z4 homo sapien
45	334	16.4	307	2 Q801T4	Q801T4 xenopus lae

ALIGNMENTS

RESULT 1
ID CIW3 HUMAN STANDARD; PRT; 394 AA.
AC O14649;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1) (Two pore potassium channel KT3.1).
DE Name=KCNK3; Synonyms=TASK, TASK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=97459932; PubMed=9312005; DOI=10.1093/emboj/16.17.5464;
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT "TASK, a human background K+ channel to sense external pH variations near physiological pH.";
RL EMBO J. 16:5464-5471(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Lopes C.M.B., Gallagher P.G., Buck M.E., Butler M.H.,
RT Goldstein S.A.N.;
RT "proton block and voltage-gating are potassium-dependent in the cardiac leak channel Kcnk3.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP ACTIVATION.
RX MEDLINE=99254548; PubMed=1031245; DOI=10.1038/8084;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+ channels.";
RL Nat. Neurosci. 2:422-426(1999).
RN [4]
RP MUTAGENESIS OF HIS-98.
RX MEDLINE=21535313; PubMed=11680614;
RA Ashmole I., Goodwin P.A., Stanfield P.R.;
RT "TASK-5, a novel member of the tandem pore K+ channel family.";
RL Pflugs Arch. 442:828-833(2001).
CC -!- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein. Rectification direction results from potassium ion concentration on either side of the membrane. Acts as an outward rectifier when external potassium concentration is low. When external potassium concentration is high, current is inward.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: Widespread expression in adult. Strongest expression in pancreas and placenta. Lower expression in brain, lung, prostate, heart, kidney, uterus, small intestine and colon.
CC -!- MISCELLANEOUS: Inhibited by external acidification. Activated by

halothane and isoflurane.
 -!- SIMILARITY: belongs to the two pore domain potassium channel
 (TC 1.A.1.8) family.

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 EMBL; AF006823; AAC51777.1; -;
 EMBL; AF065163; AAG29340.1; -;
 Genbank; HGNC:6278; KCNK3.
 MIM; 603220; -;
 GO; GO:0005887; C:integral to plasma membrane; TAS.
 GO; GO:0005267; F:potassium channel activity; TAS.
 GO; GO:0006813; P:potassium ion transport; TAS.
 GO; GO:0007268; P:synaptic transmission; TAS.
 InterPro; IPR005821; Ion trans.
 InterPro; IPR003280; K+channel_2pore.
 InterPro; IPR001622; K+channel_pore.
 InterPro; IPR005406; TASK1 channel.
 InterPro; IPR003092; TASK channel.
 Pfam; PF00520; Ion trans_1.
 PRINTS; PR01333; 2POREKCHANNEL.
 PRINTS; PR01584; TASK1CHANNEL.
 KW Glycoprotein; Ion transport; Ionic channel; Potassium;
 Potassium channel; Transmembrane; Transport; Voltage-gated channel.
 FT DOMAIN 1 8 Cytoplasmic (Potential).
 FT TRANSMEM 9 29 Potential.
 FT DOMAIN 78 101 Pore-forming 1 (Potential).
 FT TRANSMEM 108 128 Potential.
 FT DOMAIN 129 158 Cytoplasmic (Potential).
 FT TRANSMEM 159 179 Potential.
 FT DOMAIN 184 207 Pore-forming 2 (Potential).
 FT TRANSMEM 223 243 Potential.
 FT DOMAIN 244 394 Cytoplasmic (Potential).
 FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).
 FT MUTAGEN 98 98 H->N: Greatly reduces pH sensitivity.
 SQ SEQUENCE 394 AA; 43518 MW; 9FF4C8266F615FB7 CRC64;

Query Match 100.0%; Score 2042; DB 1; Length 394;
 Best Local Similarity 100.0%; Fred. NO. 1.3e-153;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRQNVRLALIVCTFTYLLVGAAPFDALSEPELIERQRLERQQLERARYNLSQGGYE 60
 DB 1 MKRQNVRLALIVCTFTYLLVGAAPFDALSEPELIERQRLERQQLERARYNLSQGGYE 60

QY 61 ELERVVRLKPKHAGVQWRFAGSFYFAITVITIGYHAAPSTDGKVCFMFYALLGIPL 120
 DB 61 ELERVVRLKPKHAGVQWRFAGSFYFAITVITIGYHAAPSTDGKVCFMFYALLGIPL 120

QY 121 TLVFMQSLGERINTLVRYLLHRAKGLGNRRADVSNMNVLIQFFSCITLCIGAAAFSH 180
 DB 121 TLVFMQSLGERINTLVRYLLHRAKGLGNRRADVSNMNVLIQFFSCITLCIGAAAFSH 180

QY 181 YEHWTFQYAYCFITLTITIGDYVALQDQALQTOPOYVAFSFVYILTLGTIVIGAFIN 240
 DB 181 YEHWTFQYAYCFITLTITIGDYVALQDQALQTOPOYVAFSFVYILTLGTIVIGAFIN 240

QY 241 LVVLRPMNTNAEDKRAHRAHLLTRNGAGGGGGGSAHTTDTTASSTAAAGGGFRNYY 300
 DB 241 LVVLRPMNTNAEDKRAHRAHLLTRNGAGGGGGGSAHTTDTTASSTAAAGGGFRNYY 300

QY 301 AEVLHFQSCSLWYKSRKLYQSPIMIIIPDLSTDCVESHSPGGGGRYSTPSSR 360
 DB 301 AEVLHFQSCSLWYKSRKLYQSPIMIIIPDLSTDCVESHSPGGGGRYSTPSSR 360

QY 361 CLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

Db 361 CLCSGAPRAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 2
 CIW3 RAT
 ID CIW3 RAT STANDARD; PRT; 411 AA.
 AC O54912;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Potassium channel subfamily K member 3 (Acid-sensitive potassium channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
 DE (Two pore potassium channel KT3.1).
 DE Name=Kcnk3; Synonyms=Taak, Task1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum;
 RX MEDLINE=98099797; PubMed=9437008;
 RA Leonoudakis D., Gray A.T., Winegar B.D., Kindler C.H., Harada M., Taylor D.M., Chavez R.A., Forsayeth J.R., Yost C.S.;
 RT "An open rectifier potassium channel with two pore domains in tandem cloned from rat cerebellum";
 RL J. Neurosci. 18:868-877(1998).
 CC -!- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein. Rectification direction results from potassium ion concentration on either side of the membrane. Acts as an outward rectifier when external potassium concentration is low. When external potassium concentration is high, current is inward (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- TISSUE SPECIFICITY: Strongest expression in heart. Moderate expression in lung and brain. Low levels in liver, kidney and skeletal muscle.
 CC -!- MISCELLANEOUS: Inhibited by extracellular acidification, zinc, bupivacaine and phenytoin. Activated by protein kinase A.
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
 CC -----
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 EMBL; AF031384; AAC39952.1; -;
 RGD; 61997; Kcnk3.
 InterPro; IPR005821; Ion trans.
 InterPro; IPR003280; K+channel_2pore.
 InterPro; IPR001622; K+channel_pore.
 InterPro; IPR005406; TASK1 channel.
 InterPro; IPR003092; TASK channel.
 Pfam; PF00520; Ion trans_1.
 PRINTS; PR01333; 2POREKCHANNEL.
 PRINTS; PR01584; TASK1CHANNEL.
 KW Glycoprotein; Ion transport; Ionic channel; Potassium;
 Potassium channel; Transmembrane; Transport; Voltage-gated channel.
 FT DOMAIN 1 8 Cytoplasmic (Potential).
 FT TRANSMEM 9 29 Potential.
 FT DOMAIN 78 101 Pore-forming 1 (Potential).
 FT TRANSMEM 108 128 Potential.
 FT DOMAIN 129 158 Cytoplasmic (Potential).
 FT TRANSMEM 159 179 Potential.
 FT DOMAIN 184 207 Pore-forming 2 (Potential).
 FT TRANSMEM 223 243 Potential.
 FT DOMAIN 244 411 Cytoplasmic (Potential).

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FT CARBOHYD 53 53 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 411 AA; 45276 MW; D2778016B09E2BF5 CRC64;

Query Match
Best Local Similarity 88.3%; Score 1850.5; DB 1; Length 411;
Matches 363; Conservative 8; Mismatches 23; Indels 17; Gaps 2;

QY 1 MKRQNVRLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSGGYE 60
DB 1 MKRQNVRLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSGGYE 60
QY 61 ELERVVRLKPKHAGVQWRFGAGFYFAITVITIGYHAAPSDGKVKFCMFYALGIGPL 120
DB 61 ELERVVRLKPKHAGVQWRFGAGFYFAITVITIGYHAAPSDGKVKFCMFYALGIGPL 120
QY 121 TLVFMFQSLGERINTLVRYLLHRAKGLGMRRAVDVSMANMVLIGFFSCISTLCIGAAAFSH 180
DB 121 TLVFMFQSLGERINTLVRYLLHRAKGLGMRRAVDVSMANMVLIGFFSCISTLCIGAAAFSH 180
QY 181 YEHWTFFQAYYYCFIITLTIGFGDYVALQKDALQTOPOQVAFSVFVILTGLTVIGAFLN 240
DB 181 YERWTFFQAYYYCFIITLTIGFGDYVALQKDALQTOPOQVAFSVFVILTGLTVIGAFLN 240
QY 241 LVVLRFTWNAEDEKDAEHRALLTNGQAGGGG-----GGSAAHTTDTASATAA- 291
DB 241 LVVLRFTWNAEDEKDAEHRALLTNGQAGGGG-----GGSAAHTTDTASATAA- 291
QY 292 -----GGGGRNRYAEVLHFQSCSLWYKREKLOYSIPMIIPRDLSTSDTCTVEOS 343
DB 292 -----GGGGRNRYAEVLHFQSCSLWYKREKLOYSIPMIIPRDLSTSDTCTVEOS 343
QY 301 GMGVGVGVGGSGFRNRYAEMLHFQSCSLWYKREKLOYSIPMIIPRDLSTSDTCTVEHS 360
DB 301 GMGVGVGVGGSGFRNRYAEMLHFQSCSLWYKREKLOYSIPMIIPRDLSTSDTCTVEHS 360
QY 344 HSPGPGGGYSDYTPSRRCILCSGAPRAISVSTGLHSLSTFRGLMKRRSSV 394
DB 344 HSPGPGGGYSDYTPSRRCILCSGAPRAISVSTGLHSLSTFRGLMKRRSSV 394
QY 361 HSPGPGGGYSDYTPSRRCILCSGAPRAISVSTGLHSLSTFRGLMKRRSSV 411
DB 361 HSPGPGGGYSDYTPSRRCILCSGAPRAISVSTGLHSLSTFRGLMKRRSSV 411

RESULT 3
CIW3_MOUSE
ID ID CIW3_MOUSE STANDARD; PRT; 409 AA.
AC O3511; O35163;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 3 (Acid-sensitive potassium
DE channel protein TASK-1) (TWIK-related acid-sensitive K+ channel 1)
DE (Cardiac two-pore background K+ channel) (CTBAK-1) (Two pore potassium
DE channel KT3.1).
GN Name-Kcnk3; Synonyms=CtbaK, TASK, Task1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=98165556; PubMed=9506712;
RA Kim D., Fujita A., Horio Y., Kurachi Y.;
RT "Cloning and functional expression of a novel cardiac two-pore
RT background K+ channel (CTBAK-1).";
RL Circ. Res. 82:513-518 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=20287574; PubMed=10748056; DOI=10.1074/jbc.M001948200;
RA Lopes C.M., Gallagher P.G., Buck M.E., Butler M.H., Goldstein S.A.;
RT "Proton block and voltage gating are potassium-dependent in the
RT cardiac leak channel Kcnk3.";
RL J. Biol. Chem. 275:16969-16978 (2000).
RN [3]
RP SEQUENCE OF 4-409 FROM N.A.
RX MEDLINE=97459932; PubMed=9312005; DOI=10.1093/emboj/16.17.5464;
RA Duprat F., Lesage F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;
RT "TASK, a human background K+ channel to sense external pH variations
```

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RT near physiological pH.";
RL EMBO J. 16:5464-5471 (1997).
CC -I- FUNCTION: pH-dependent, voltage-insensitive, background potassium
CC channel protein. Rectification direction results from potassium
CC ion concentration on either side of the membrane. Acts as an
CC outward rectifier when external potassium concentration is low.
CC When external potassium concentration is high, current is inward
CC (by similarity).
CC -I- SUBUNIT: Homodimer (Potential).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -I- TISSUE SPECIFICITY: Very strong expression in heart, also detected
CC in kidney, brain, skin, testis, lung, skeletal muscle, small
CC intestine and stomach. Not detected in liver, thymus or spleen.
CC -I- MISCELLANEOUS: Inactivated by barium.
CC -I- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AB008537; BAA25436.1; -
CC EMBL; AF241798; AAF81418.1; -
CC EMBL; AF242508; AAF81418.1; JOINED.
CC EMBL; AF065162; AAG29339.1; -
CC EMBL; AF006824; AAC53367.1; -
CC EMBL; AB013345; BAA28349.1; -
CC MGD; MGI:1100509; Kcnk3.
CC InterPro; IPR005821; Ion trans.
CC InterPro; IPR003280; K+channel_2pore.
CC InterPro; IPR001622; K+channel_pore.
CC InterPro; IPR005406; TASK1_channel.
CC InterPro; IPR003092; TASK_channel.
CC Pfam; PF00520; Ion trans; 1.
CC PRINTS; PR01333; 2POREKCHANEL.
CC PRINTS; PR01584; TASK1CHANNEL.
CC PRINTS; PR01095; TASKCHANNEL.
CC Glycoprotein; Ion transport; Ionic channel; Potassium;
CC Potassium channel; Transmembrane; Transport; Voltage-gated channel.
CC DOMAIN 1 8 Cytoplasmic (Potential).
CC TRANSMEM 9 29 Pore-forming 1 (Potential).
CC DOMAIN 78 101 Potential.
CC TRANSMEM 108 128 Cytoplasmic (Potential).
CC DOMAIN 129 158 Potential.
CC TRANSMEM 159 179 Pore-forming 2 (Potential).
CC DOMAIN 184 207 Potential.
CC TRANSMEM 223 243 Cytoplasmic (Potential).
CC DOMAIN 244 409 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 53 53
CC CONFLICT 4 4 Q -> E (in Ref. 3).
CC CONFLICT 123 123 V -> I (in Ref. 3).
CC SEQUENCE 409 AA; 45068 MW; 35236E011AAC5687 CRC64;
SQ

Query Match
Best Local Similarity 88.5%; Score 1840.5; DB 1; Length 409;
Matches 362; Conservative 7; Mismatches 25; Indels 15; Gaps 2;

QY 1 MKRQNVRLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSGGYE 60
DB 1 MKRQNVRLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQELRARNYLSGGYE 60
QY 61 ELERVVRLKPKHAGVQWRFGAGFYFAITVITIGYHAAPSDGKVKFCMFYALGIGPL 120
DB 61 ELERVVRLKPKHAGVQWRFGAGFYFAITVITIGYHAAPSDGKVKFCMFYALGIGPL 120
QY 121 TLVFMFQSLGERINTLVRYLLHRAKGLGMRRAVDVSMANMVLIGFFSCISTLCIGAAAFSH 180
DB 121 TLVFMFQSLGERINTLVRYLLHRAKGLGMRRAVDVSMANMVLIGFFSCISTLCIGAAAFSH 180
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QY 181 YEHWTFFQAYYYCFITLTTTIGFDYVALQKQALQTOPOYVAFSVFYILTGLTVIGAFIN 240
|||
DB 181 YERWTFQAYYYCFITLTTTIGFDYVALQKQALQTOPOYVAFSVFYILTGLTVIGAFIN 240
|||
QY 241 LVVLRFTMTNABDEKRAEHRALLTRNGQAGGGG-----GSAHTTDTASSTAAA- 291
|||
DB 241 LVVLRFTMTNABDEKRAEHRALLTRNGQAGGGG-----GSAHTTDTASSTAAA- 291
|||
QY 292 -----GGGGRNVAEVLHFQSMCCLWYKREKLOYSIPIIIPRDLSTSDTCVQSHS 345
|||
DB 301 GVGVGVGSGGRNVAEVLHFQSMCCLWYKREKLOYSIPIIIPRDLSTSDTCVQSHS 360
|||
QY 346 SPGGGGRYSDTPSRRLCSCGAPRSALSSVSTGLHSLSTFRGLMKRRSSV 394
|||
DB 361 SPGGGGRYSDTPSRRLCSCGAPRSALSSVSTGLHSLSTFRGLMKRRSSV 409
|||

RESULT 4
Q9ESM5 PRELIMINARY; PRT; 392 AA.
AC Q9ESM5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE TASK1 splice bvariant (TASK1b).
GN Name-KCNK3b;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Brain;
RA Ohya S., Kitsukawa M., Imaizumi Y.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
(CC 1.A.1.8) family.
DR EMBL; AB048823; BAB16710.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005406; TASK1 channel.
DR InterPro; IPR003092; TASK channel.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01333; 2FORECHANNEL.
DR PRINTS; PR01584; TASK1CHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 392 AA; 43150 MW; F5438B12AAD7FB1B CRC64;

Query Match 84.8%; Score 1732; DB 2; Length 392;
Best Local Similarity 83.9%; Pred. No. 4.8e-129;
Matches 345; Conservative 7; Mismatches 23; Indels 36; Gaps 4;

QY 1 MKRQNVRLALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARNYLSGGGYE 60
|||
DB 1 MKRQNVRLALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARNYLSGGGYE 60
|||

QY 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYHAAPSTDGKVKFCMFYALLGIPL 120
|||
DB 42 ELERVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYHAAPSTDGKVKFCMFYALLGIPL 101
|||

QY 121 TLVMFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVLIGFSCISTLCIGAAAFPSH 180
|||
DB 102 TLVMFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVLIGFSCISTLCIGAAAFPSH 161
|||

QY 181 YEHWTFFQAYYYCFITLTTTIGFDYVALQKQALQTOPOYVAFSVFYILTGLTVIGAFIN 240
|||
```

```
DB 162 YERWTFQAYYYCFITLTTTIGFDYVALQKQALQTOPOYVAFSVFYILTGLTVIGAFIN 221
|||
QY 241 LVVLRFTMTNABDEKRAEHRALLTRNGQAGGGG-----GSAHTTDTASSTAAA- 291
|||
DB 241 LVVLRFTMTNABDEKRAEHRALLTRNGQAGGGG-----GSAHTTDTASSTAAA- 291
|||
QY 292 -----GGGGRNVAEVLHFQSMCCLWYKREKLOYSIPIIIPRDLSTSDTCVQSHS 343
|||
DB 282 GMVGVGVGSGGRNVAEVLHFQSMCCLWYKREKLOYSIPIIIPRDLSTSDTCVQSHS 341
|||
QY 344 HSPGGGGRYSDTPSRRLCSCGAPRSALSSVSTGLHSLSTFRGLMKRRSSV 394
|||
DB 342 HSPGGGGRYSDTPSRRLCSCGAPRSALSSVSTGLHSLSTFRGLMKRRSSV 392
|||

RESULT 5
Q9QX34 PRELIMINARY; PRT; 299 AA.
AC Q9QX34;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Putative potassium channel DP4 (Fragment).
GN Name-Kcnk3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Gan L., Joiner W.J., Quinn A.M., Wang L.-Y., Hughes T.,
RA Kaczmarek L.K.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
(CC 1.A.1.8) family.
DR EMBL; AF022821; AAD09338.1; -.
DR MGD; MGI:1100509; Kcnk3.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005406; TASK1 channel.
DR InterPro; IPR003092; TASK channel.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01333; 2FORECHANNEL.
DR PRINTS; PR01584; TASK1CHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 299
SQ SEQUENCE 299 AA; 33325 MW; DCD41D8A212939C4 CRC64;

Query Match 65.3%; Score 1333; DB 2; Length 299;
Best Local Similarity 88.9%; Pred. No. 1.6e-97;
Matches 263; Conservative 7; Mismatches 18; Indels 8; Gaps 1;

QY 4 QNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARNYLSGGGYE 63
|||
DB 2 ENVRTALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARNYLSGGGYE 61
|||

QY 64 RVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYHAAPSTDGKVKFCMFYALLGIPLTV 123
|||
DB 62 RVVLRKPKHAGVQWRPAGSFYFAITVITTTIGYHAAPSTDGKVKFCMFYALLGIPLTV 121
|||

QY 124 MFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVLIGFSCISTLCIGAAAFPSH 183
|||
DB 122 MFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVLIGFSCISTLCIGAAAFPSH 181
|||

QY 184 WTFQAYYYCFITLTTTIGFDYVALQKQALQTOPOYVAFSVFYILTGLTVIGAFINLVV 243
|||
DB 182 WTFQAYYYCFITLTTTIGFDYVALQKQALQTOPOYVAFSVFYILTGLTVIGAFINLVV 241
|||
```

QY 244 LRPMWNAEDKDAEHRALLTNGQAGGGG-----GCSAHTTDTASSTAAA 291
 |||||
 Db 242 LRPMWNAEDKDAEHRALLTNGQAVGLGSLGSLGSGVGRPRDPVTCAAA 297
 |||||

RESULT 6

Q9ESM4 PRELIMINARY; PRT; 301 AA.
 ID Q9ESM4
 AC Q9ESM4
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE TWIK-related acid-sensitive K⁺ channel splice variant (TASK1c).
 GN Name=CKNK3c;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Aorta;
 RA Ohya S., Kitsukawa M., Imaizumi Y.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 EMBL: AB048824; BAB16711.1; --
 DR GO: 0016021; C: integral to membrane; IEA.
 DR GO: 0005216; F: ion channel activity; IEA.
 DR GO: 0005267; F: potassium channel activity; IEA.
 DR GO: 0006813; P: potassium ion transport; IEA.
 DR InterPro: IPR001623; K+ channel pore.
 DR InterPro: IPR005406; TASK1 channel.
 DR InterPro: IPR003092; TASK channel.
 DR PRINTS; PRO1584; TASK1CHANNEL.
 DR PRINTS; PRO1095; TASKCHANNEL.
 KW Ionic channel.
 SQ SEQUENCE 301 AA; 32811 MW; 265DE38DFA79595E CRC64;

Query Match 63.8%; Score 1298.5; DB 2; Length 301;
 Best Local Similarity 85.0%; Pred. No. 8.6e-95;
 Matches 256; Conservative 6; Mismatches 22; Indels 17; Gaps 2;

QY 111 MFVALLGIPLTVMFQSLGERINTLVYLLHRAKGLGMRADVSMANNVLIGFSCIST 170
 |||||
 Db 1 MFVALLGIPLTVMFQSLGERINTLVYLLHRAKGLGMRADVSMANNVLIGFVSCIST 60
 |||||
 QY 171 LCIGAAAFSHYEWTFQAYYYCFITLTIGFDYVALQDQALQTPQVAFSFYIILT 230
 |||||
 Db 61 LCIGAAAFSYERWTFQAYYYCFITLTIGFDYVALQDQALQTPQVAFSFYIILT 120
 |||||
 QY 231 GLTVIGAFNLVLRPMTWNAEDKDAEHRALLTNGQAGGGG-----GCSAHTT 282
 |||||
 Db 121 GLTVIGAFNLVLRPMTWNAEDKDAEHRALLTNGQAGGIGLGLSCLSGSLGSGVGRPR 180
 |||||
 QY 283 DTASSTAAA-----GGGPRNYVAEVLHQSCLWYKREKLOYSPIMTIPDL 333
 |||||
 Db 181 DPVTCAAAAGMGVGVGGSGPRNYAEMLHQSCLWYKREKLOYSPIMTIPDL 240
 |||||
 QY 334 STSDTCVEQSHSPGGGGRYSDTPSRCLCSGAPRAISSVSTGLSHLSLTFGLMKRRSS 393
 |||||
 Db 241 STSDTCVEHSHSPGGGGRYSDTPSPCLCSGTQRAISSVSTGLSHLSLTFGLMKRRSS 300
 |||||
 QY 394 V 394
 |||||
 Db 301 V 301

RESULT 7

Q63Z10 PRELIMINARY; PRT; 374 AA.
 ID Q63Z10
 AC Q63Z10
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RA Klein S., Gerhard D.S.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC082937; AAH82937.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 374 AA; 42718 MW; 8F37D8FF1F689F63 CRC64;

Query Match 56.3%; Score 1150; DB 2; Length 374;
 Best Local Similarity 59.6%; Pred. No. 6.6e-83;
 Matches 235; Conservative 47; Mismatches 92; Indels 20; Gaps 4;

QY 1 MKRQNVRLALIVCTFTYLLVGAAVFDALSEPELIERORLELRQCELARVNLISGGYE 60
 |||||
 Db 1 MKRQNVRLSLICITFTYLLVGAAVFDALSEYEWREKLEKAEIRLKGKYNISSEYR 60
 |||||
 QY 61 ELERVVLKPKHAGVQWRPAGSFYFAITVITIGYHAASTPDGKVKFCMFYALIGIPL 120
 |||||
 Db 61 QLELVIMQSEPHRAGVQWRPAGSFYFAITVITIGYHAASTPDGKVKFCMFYALIGIPL 120
 |||||
 QY 121 TLVVFQSLGERINTLVYLLHRAKGLGMRADVSMANNVLIGFSCISTLCIGAAAFSH 180
 |||||
 Db 121 TLVVFQSLGERINTLVYLLHRAKGLGMRADVSMANNVLIGFSCISTLCIGAAAFSH 180
 |||||
 QY 181 YEHWTFFQAYYYCFITLTIGFDYVALQDQALQTPQVAFSFYIILTGLTVIGAFNL 240
 |||||
 Db 181 YEENFFQAYYYCFITLTIGFDYVALQDQALQTPQVAFSFYIILTGLTVIGAFNL 240
 |||||
 QY 241 LVVLRPMTWNAEDKDAEHRALLTNGQAGGGGSAHTTDTASSTAAAGGGGPRNVY 300
 |||||
 Db 241 LVVLRPMTWNAEDKDAEHRALLTNGQAGGGGSAHTTDTASSTAAAGGGGPRNVY 300
 |||||
 QY 301 AEVLHQSCLWYKREKLOYSPIMTIPDLSTSDTCVEQSHSPGGGGRYSDTPSR 360
 |||||

Db 288 ABVTLQSVSCMCYRSHE---YTRSMVSHQNSFSLNPOYFHSISYKIBESPTLKN 344

Qy 361 CLCSGAPRSATSSVSTGLHSLSTFGLMKRRSSV 394

Db 345 SLFP-----SPVSSVSGFLHSLFTDKHRLMKRRKSI 374

RESULT 8

CIW9 HUMAN

ID C9N9C2; STANDARD; PRT; 374 AA.

AC Q9N9C2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 9 (Acid-sensitive potassium channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3)

DE (Two pore potassium channel KT3.2).

DE Name=KCNK9; Synonyms=TASK3;

GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

OX [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20287530; PubMed=10747866; DOI=10.1074/jbc.M000030200;

RA Rajan S., Wischmeyer E., Liu G.X., Preisig-Mueller R., Daut J., Karschin A., Derst C.,

RA "TASK-3, a novel tandem pore domain acid-sensitive K+ channel. An extracellular histidine as pH sensor";

RT J. Biol. Chem. 275:16650-16657 (2000).

RL [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Cerebellum;

RC PubMed=11042359; DOI=10.1016/S0169-328X(00)00183-2;

RX Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M., Kellell R.E., Murdoch P.R., Randall A.D., Rennie G.I., Gloger I.S.;

RT "Cloning, localisation and functional expression of a novel human, cerebellum specific, two pore domain potassium channel.";

RL Brain Res. Mol. Brain Res. 82:74-83 (2000).

RN [3]

RP SEQUENCE FROM N.A.

RA Girard C., Lesage F., Tinel N., Lazdunski M.;

RT "Human Task-3, a novel 2p domain potassium channel related to Task.";

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=21324619; PubMed=11431495;

RA Vega-Saenz de Miera E., Lau D.H.P., Zhadina M., Pountney D., Coetzee W.A., Rudy B.;

RA "KT3.2 and KT3.3, two novel human two-pore K(+) channels closely related to TASK-1.";

RT J. Neurophysiol. 86:130-142 (2001).

RL -!- FUNCTION: pH-dependent, voltage-insensitive, background potassium channel protein.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: Mainly found in the cerebellum. Also found in adrenal gland, kidney and lung.

CC -!- MISCELLANEOUS: Inhibited by phorbol 12-myristate 13-acetate (PMA). Insensitive to changes in the pH range of 7-8.

CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

CC -----

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CC -----

CC EMBL; AF212829; AAF63708.1; -.

DR EMBL; AF248241; AAG31730.1; -.

DR EMBL; AF279809; AAF85982.1; -.

DR EMBL; AF257080; AAG33126.1; -.

DR Genew; HGNC:6283; KCNK9.

DR MIM; 605874; -.

DR GO; GO:0005624; C:membrane fraction; NAS.

DR GO; GO:0005267; P:potassium channel activity; NAS.

DR GO; GO:0006813; P:potassium ion transport; NAS.

DR InterPro; IPR005821; Ion trans.

DR InterPro; IPR003280; K+channel 2pore.

DR InterPro; IPR001622; K+channel pore.

DR InterPro; IPR005407; TASK3 channel.

DR InterPro; IPR003092; TASK channel.

DR Pfam; PF00520; Ion trans; 1.

DR PRINTS; PR01333; 2PORECHANNEL.

DR PRINTS; PR01585; TASK3CHANNEL.

DR PRINTS; PR01095; TASKCHANNEL.

DR Glycoprotein; Ion transport; Ionic channel; Potassium; Potassium channel; Transmembrane; Transport; Voltage-gated channel.

KW Potassium channel; Transmembrane; Transport; Voltage-gated channel.

FT DOMAIN 1 8 Cytoplasmic (Potential).

FT TRANSMEM 9 29 Pore-forming 1 (Potential).

FT DOMAIN 78 101 Pore-forming 1 (Potential).

FT TRANSMEM 108 128 Cytoplasmic (Potential).

FT DOMAIN 129 158 Cytoplasmic (Potential).

FT TRANSMEM 159 179 Pore-forming 2 (Potential).

FT DOMAIN 184 207 Pore-forming 2 (Potential).

FT TRANSMEM 219 239 Potassium channel.

FT DOMAIN 240 374 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 53 53

SQ SEQUENCE 374 AA; 42263 MW; 8A19AE5EA4D7F38 CRC64;

Query Match 54.7%; Score 1116; DB 1; Length 374;

Best Local Similarity 59.0%; Pred. No. 3.3e-80;

Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

Qy 1 MKRQVRLALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARVNLSSGGVE 60

Db 1 MKRQVRLSLIVCTFTYLLVGAADFDALESDHEEKEKAEIRIKGTINISSEYR 60

Qy 61 ELERVVLRLKPKAGVQWRFAGSFYFAITVTITTYGYHAAPSTDGKVFYALLGIPL 120

Db 61 QLELVILQSEPHRAGVQWKFAGSFYFAITVTITTYGYHAAPSTDGKVFYALLGIPL 120

Qy 121 TLVNFQSLGERINTLVRLHRAKGLGMRADVSMANVLIGFPSCSTLCIGAAAFSH 180

Db 121 TLVNFQSLGERMNTFVRLKRIKKCCQMRNTDSMENNVTGVFFSCMTGLCIGAAAFSQ 180

Qy 181 YEHWTFFQAYYYCRTLITIGFDYVALQDQALQTOPOYVAFSFVYILTGLTVIGAFLN 240

Db 181 CEESWFFHAYYYCFTLTITIGFDYVALQTKALQKPLVYAFSPYILVGLTVIGAFLN 240

Qy 241 LVVLRFTMTNAEDEKRAEHRALLTRNQAGGGGGGSAHTTDTTASSTAAGGGGFRNYY 300

Db 241 LVVLRFTMTNSEDERRDAERASL-----AGNRNSMWIHIPEERPS-----RPRY 286

Qy 301 -AEVLHFQSMCCLWYKSLREKLYQVSIPIIIPDLSTSDTCVEQSHSSPGGGRYSDTFSR 359

Db 287 KADVPDLQVCSCTCYRSQD---YGGRSVAPQNSFSAKLAPHYFHSISYKIBESPTLTK 343

Qy 360 RCLCSGAPRSATSSVSTGLHSLSTFGLMKRRSSV 394

Db 344 NSLFP-----SPVSSVSGFLHSLFTDKHRLMKRRKSV 374

RESULT 9

CIW9 CAVPO

ID C9V9C2; STANDARD; PRT; 365 AA.

AC Q9V9C2;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 9 (Acid-sensitive potassium channel protein TASK-3) (TWIK-related acid-sensitive K+ channel 3).

DE Name=KCNK9; Synonyms=TASK3;

GN Cavia porcellus (Guinea pig).


```

ID Q9JLD4 PRELIMINARY; PRT; 395 AA.
AC Q9JLD4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Potassium channel TASK3.
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA MEDLINE=20200422; PubMed=10734076; DOI=10.1074/jbc.275.13.9340;
RA Kim Y., Bang H., Kim D.;
RT "TASK-3, a New Member of the Tandem Pore K+ Channel Family.";
RL J. Biol. Chem. 275:9340-9347(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Cerebellum;
RA Kim Y.M., Bang H.W., Kim D.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: Belongs to the two pore domain potassium channel
    (TC 1.A.1.8) family.
DR EMBL; AF192366; AAF60229.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0005216; P: ion channel activity; IEA.
DR GO; GO:0005267; P: potassium channel activity; IEA.
DR GO; GO:0006811; P: ion transport; IEA.
DR GO; GO:0006813; P: potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005407; TASK3_channel.
DR InterPro; IPR003092; TASK3_channel.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01333; 2POREKCHANNEL.
DR PRINTS; PR01585; TASK3CHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 395 AA; 44365 MW; 3F76F923A3AFC76 CRC64;

Query Match 47.0%; Score 960.5; DB 2; Length 395;
Best Local Similarity 69.7%; Pred. No. 7.6e-68;
Matches 186; Conservative 31; Mismatches 49; Indels 1; Gaps 1;

QY 1 MKRQVRLALIVCTFTLLVGAAVFDALSEPELIERQRLRQOELRARNYLSQGGYE 60
Db 1 MKRQVRLTSLTACTFTLLVGAAVFDALSDHEMREBEKLKABEVRLRGKYNISDDYQ 60

QY 61 ELERVVLRLKPHKAGVQVRFAGSFYFALTIVTTIGYGAAPSTDGKVPFCMFYALLGIPL 120
Db 61 QLELVILQSEPHRAGVQVRFAGSFYFALTIVTTIGYGAAPSTDGKAFPCMFYAVLGIPL 120

QY 121 TLVVFQSLGERINTLVRYLLHRAKGLGMRRADSVNANNVLTGFFSCISTLCIGAAAFSH 180
Db 121 TLVVFQSLGERNNTFVRYLLKXIKKCCGNGNTEVSMNNTVGFSCWG-LVPWAAASQ 179

QY 181 YEHWTFFQAYYYCFITLTITIGFDVVALQKQALQTPQOYVAFSVYILTGLTVTGAFIN 240
Db 180 CEDWSFFHAYYYCFITLTITIGFDVVALQKQALQKPPYAFSVYILVGLTVTGAFIN 239

QY 241 LVVLFMTMNAEDKRDRAHRLATRN 267
Db 240 LVVLFRLTMTNDEDLLEGEVAQILAGN 266

RESULT 12
CIW9_RAT
ID CIW9_RAT
AC Q9ES08;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 9 (Acid-sensitive potassium
channel protein TASK-3) (Two pore potassium channel KT3.2) (Fragment).
GN Name=Kcnk9; Synonyms=Task3;
OS Rattus norvegicus (Rat).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA MEDLINE=21324619; PubMed=11431495;
RA Vega-Saenz de Miera E., Lau D.H.P., Zhadina M., Pountney D.,
RA Coetzee W.A., Rudy B.;
RT "Kt3.2 and kt3.3, two novel human two-pore k(+) channels closely
related to TASK-1.";
RL J. Neurophysiol. 86:130-142(2001).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=21624462; PubMed=11749039; DOI=10.1006/mcne.2001.1045;
RA Karschin C., Wischmeyer E., Preisig-Mueller R., Rajan S., Derst C.,
RA Grzeschik K.-H., Daut J., Karschin A.;
RT "Expression pattern in brain of TASK-1, TASK-3, and a tandem pore
domain K(+) channel subunit, TASK-5, associated with the central
auditory nervous system.";
RL Mol. Cell. Neurosci. 18:632-648(2001).
CC -! FUNCTION: pH-dependent, voltage-insensitive, background potassium
channel protein.
CC -! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -! TISSUE SPECIFICITY: Expressed in the CNS but not in heart, lung,
liver, kidney, intestine and skeletal muscle. The highest
expression was found in the olfactory nuclei, piriform cortex,
cerebellum, antedorsal thalamic nucleus, pontine nucleus, dorsal
raphe and several nuclei in the medulla. Shows a non-homogeneous
distribution in the hippocampus. Expressed at highest levels in
the lateral posterior and inferior portions and at medium levels
in neocortex.
CC -! SIMILARITY: Belongs to the two pore domain potassium channel
(TC 1.A.1.8) family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
DR EMBL; AF257082; AAG33128.1; -.
DR RGD; 621451; Kcnk9.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR005407; TASK3_channel.
DR InterPro; IPR003092; TASK3_channel.
DR PRINTS; PR01333; 2POREKCHANNEL.
DR PRINTS; PR01585; TASK3CHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Glycoprotein; Ion transport; Ionic channel; Potassium;
Potassium channel; Transmembrane; Transport; Voltage-gated channel.
FT DOMAIN 1 8
FT TRANSMEM 9 29
FT DOMAIN 78 101
FT DOMAIN 108 128
FT DOMAIN 129 158
FT TRANSMEM 159 179
FT DOMAIN 184 207
FT TRANSMEM 219 >237
FT CARBOHYD 53 53
FT NON_TER 237 237
SQ SEQUENCE 237 AA; 26674 MW; A44D2D32BE08A7DB CRC64;

Query Match 45.2%; Score 924; DB 1; Length 237;
Best Local Similarity 73.4%; Pred. No. 3.3e-65;
```



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RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG WormBase Consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Murray J., Wohldmann P., O'Neal D.;
RA "The sequence of C. elegans cosmid F34D6.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Waterston R.;
RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX Wilson R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX WormBase Consortium;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX Wang Z.-W., Salkoff L.;
RA Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RX MEDLINE=22896676; PubMed=14534247;
RA de la Cruz I.P., Levin J.Z., Cummins C., Anderson P., Horvitz H.R.;
RT "sup-9, sup-10, and unc-93 may encode components of a two-pore K+
RT channel that coordinates muscle contraction in Caenorhabditis
RT elegans.";
RL J. Neurosci. 23:9133-9145(2003).
RN [8]
RP SEQUENCE FROM N.A.
RA Perez de la Cruz I., Horvitz H.R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
DR EMBL; AF025454; AAC71151.2; -.
DR EMBL; AF083652; AAC32863.1; -.
DR EMBL; AY357729; AAC84518.1; -.
DR PIR; T32347; T32347.
DR PIR; T43509; T43509.
DR WormBase; WBGene0006318; sup-9.
DR WormPep; F34D6.3; CE28297.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003092; TASK channel.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01333; 2FOREKCHANNEL.
DR PRINTS; PR01095; TASKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 329 AA; 36992 MW; 338A6D9A577464CD CRC64;
```

Query Match 40.2%; Score 820; DB 2; Length 329;
Best Local Similarity 48.3%; Pred. No. 8 5e-57;
Matches 172; Conservative 54; Mismatches 84; Indels 46; Gaps 7;

QY 1 MKRQNVRLALIVCTTLLVGAADFALAESEPELIERQRLRQQLRARNVLSQGGYE 60

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Db 1 MKRQNVRLALIVCTTLLVGAADFALAESEPELIERQRLRQQLRARNVLSQGGYE 60
QY 61 ELERVVLRKPKHAGVQWRFAGSFYFAITVITTTIGYCHAAPSTDGKVFQCMFYALIGIPL 120
Db 61 ILEATIVKSVPHKAGVQWRFAGSFYFAITVITTTIGYGHSTPMTDAGKVFQCMFYALAGIPL 120
QY 121 TLVWFQSLGERINTLVRYLLHRAKGLGMRRADVSMANMVLIGFFSCISTLCI--GAAAF 178
Db 121 GLIMFQSIGERMNTFAAKLLRFRRAAG-KQPIVTSDDLII--FCTGWGGLLIFGGAFMF 177
QY 179 SHVEHWTFQAYYYCFITLTITTTIGFDYVALQDQALQTOPOYVARSFVYITLGLTVIGAF 238
Db 178 SSTENWTFDAVYCFVITTTITTTIGFDYVALQKRGSLQTOPEYVFFSLVFLFGLTVISAA 237
QY 239 LNLVLRFMNTMAEDEKRDAAEHRAL-----LTRNGQAGGGGGGSAHTTTDTASTAAAGGG 294
Db 238 MNLVLRFLTMNTEDEERDEQEAIIAAQGLVVRVGDPTADDGFLPLSDNVSLAS----- 292
QY 295 GFRNVYAEVLHFQSMCSCMLWYKSRKQLQYSIPMIIPRDLSTSDTCVEQSHSSPGGG 350
Db 293 -----CSC-YQLPDEKLRHR-----HRKHTEPHGG 316
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Search completed: July 13, 2005, 08:44:33
Job time : 92.0757 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 07:58:54 ; Search time 97.2039 Seconds
(without alignments)
1567.669 Million cell updates/sec

Title: US-09-503-089A-5
Perfect score: 2042
Sequence: 1 MKRQVRRLALIVCTFYLL.....STGLHSLSTFRLMKRRSSV 394

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_16Dec04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2042	100.0	394	3	AAE10343 Murine TA
2	2042	100.0	394	3	Aay79674 Human pot
3	2042	100.0	394	3	Aay87291 Human sig
4	2042	100.0	394	8	Adi27924 Human pro
5	2042	100.0	394	8	Adi27925 Human pro
6	2042	100.0	395	8	Adi27915 Human pro
7	1850.5	90.6	412	8	Adi27916 Rat prote
8	1819	89.1	405	3	Aay95230 Mouse pot
9	1235.5	60.5	309	4	Aau07620 Mouse 2P
10	1116	54.7	374	3	Aab18807 Amino aci
11	1116	54.7	374	3	Aab18813 Protein e
12	1116	54.7	374	4	Aag63938 Amino aci
13	1116	54.7	374	5	Aae13279 Human tra
14	1116	54.7	374	5	Aae22989 Human TWI
15	1116	54.7	374	8	Adi27948 Human TWI
16	1116	54.7	376	8	Adi27925 Human pro
17	1116	54.7	376	8	Adi27915 Human pro
18	846	41.4	330	7	ADB80478 Ovarian c
19	846	41.4	400	4	Aae10679 Human TWI
20	846	41.4	400	8	Adi27912 Human TWI
21	838	41.0	330	4	AAB47334 FCTR11. 8
22	838	41.0	330	7	ADK18422 Human NOV
23	838	41.0	400	4	Aae10678 Human TWI
24	838	41.0	400	5	Aae13286 Human tra
25	838	41.0	400	8	Adi27909 Human TWI

26	785.5	38.5	436	4	ABG29273	Abg29273 Novel hum
27	777	38.1	340	4	ABB64375	Abb64375 Drosophi
28	774	37.9	279	4	AAM14676	Aam14676 Peptide #
29	774	37.9	279	4	ABB33636	Abb33636 Peptide #
30	774	37.9	279	4	AAM27095	Aam27095 Peptide #
31	774	37.9	279	4	ABB28454	Abb28454 Peptide #
32	774	37.9	279	4	ABB19091	Abb19091 Protein #
33	774	37.9	279	4	AAM66810	Aam66810 Human bon
34	774	37.9	279	4	AAM54409	Aam54409 Human bra
35	774	37.9	279	4	ABG48478	Abg48478 Human liv
36	774	37.9	279	4	AAM02399	Aam02399 Peptide #
37	774	37.9	279	5	ABG36465	Abg36465 Human pep
38	773	37.9	408	4	AAB31804	Aab31804 Amino aci
39	742	36.3	398	4	ABO17187	Abb17187 Drosophi
40	619	30.3	212	6	ABO14995	ABO14995 Human NOV
41	379	18.6	361	4	AAB31805	Aab31805 Amino aci
42	373	18.3	491	8	ABO84626	ABO84626 Mouse can
43	370	18.1	411	3	AAE10342	Aae10342 Murine TR
44	369	18.1	370	2	AAy30648	Aay30648 A mechani
45	369	18.1	411	2	AAy28497	Aay28497 Mouse h-T

ALIGNMENTS

RESULT 1
AAE10343
ID AAE10343 standard; protein; 394 AA.

AC AAE10343;
XX
DT 10-DEC-2001 (first entry)
XX
DE Murine TASK potassium channel protein.
XX
KW Murine; potassium channel protein; TREK-1; TASK; anaesthetic; analgesia;
XX
OS Mus sp.
XX
PN WO200047738-A2.
XX
PD 17-AUG-2000.

XX
PF 11-FEB-2000; 2000WO-IB0000226.
XX
PR 12-FEB-1999; 99US-0119727P.
PR 11-FEB-2000; 2000US-00503089.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;
WPI; 2000-549146/50.
XX
PT Novel nucleic acid encoding a TREK-1 potassium channel protein for
transfecting cells to be used to identify compounds with anesthetic
properties.
XX
PS Claim 23; Page 34-35; 39pp; English.
XX
CC The invention relates to human and mouse TREK-1 potassium channel
proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
useful for transfecting cells to induce expression of the TREK-1
potassium channel protein. These cells are then used in assays to
identify compounds which have anaesthetic properties, producing a safe,
reversible state of unconsciousness with concurrent amnesia and analgesia
in a mammal upon inhalation. The present sequence is murine TASK
potassium channel protein related to the invention
SQ Sequence 394 AA;

Query Match 100.0%; Score 2042; DB 3; Length 394;

KW reproductive disorder; developmental disorder; arteriosclerosis;
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
 KW Parkinson's disease; Huntington's diseases; ovulatory defect;
 KW muscular dystrophy.
 XX Homo sapiens.
 XX WO200000610-A2.
 XX 06-JAN-2000.
 XX 25-JUN-1999; 99WO-US014484.
 XX 26-JUN-1998; 98US-0090762P.
 XX 31-JUL-1998; 98US-0094983P.
 XX 01-OCT-1998; 98US-0102686P.
 XX 11-DEC-1998; 98US-0112129P.
 XX (INCY-) INCYTE PHARM INC.
 XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;
 PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;
 PI Bandman O;
 XX WPI; 2000-160673/14.
 XX N-PSDB; AA298176.
 XX New human signal peptide-containing proteins useful in treatment,
 PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular
 PT disease.
 XX Claim 1; Page 207-208; 327pp; English.
 XX AA298109 to AA298242 encode AAY87224 to AAY87357 which represent the
 CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have
 CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can be
 CC used in gene therapy. HSPs can be used to treat or prevent disorders
 CC associated with decreased activity or function of HSP. Antagonists of
 CC HSP are used to treat or prevent disorders associated with increased
 CC activity or function of HSP. Such diseases include cell proliferation
 CC (including cancer), inflammation, cardiovascular, neurological,
 CC reproductive or developmental disorders, (e.g. arteriosclerosis,
 CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
 CC asthma, Crohn's disease, microbial or other infections, congestive or
 CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
 CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
 CC nucleic acids can be used for the recombinant production of HSP, for
 CC detecting HSP in standard hybridisation and amplification assays (for
 CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming
 CC or ribozyme therapeutics, for detecting related sequences or genetic
 CC variations, and for chromosomal mapping. HSP are also used to raise
 CC specific antibodies (Ab) and to screen for agonists and antagonists
 CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP
 CC -related diseases (in usual immunoassays), as therapeutic antagonists, in
 CC competitive drug screens, and for purification of HSP from natural
 CC sources
 XX Sequence 394 AA;
 SQ
 Query Match 100.0%; Score 2042; DB 3; Length 394;
 Best Local Similarity 100.0%; Pred. No. 5.3e-213;
 Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKRQVRLALIVCTTLLVGAAPDALESEPELIERQRLRQELRARNLSGGYE 60
 DB 1 MKRQVRLALIVCTTLLVGAAPDALESEPELIERQRLRQELRARNLSGGYE 60
 QY 61 ELERVVRLKPKHAGVQWRFAGSFYFAITVITIGYGAAPSTDDGKVCFMFALLIGIPL 120
 DB 61 ELERVVRLKPKHAGVQWRFAGSFYFAITVITIGYGAAPSTDDGKVCFMFALLIGIPL 120

QY 121 TLVWFQSLGERINTLVRYLLHRAKKGLMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
 DB 121 TLVWFQSLGERINTLVRYLLHRAKKGLMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
 QY 181 YEHWTFFQAYYYCFITLTITIGFDYVALQDQALQTOPOYVAFSFVYILTGLTVIGAFLN 240
 DB 181 YEHWTFFQAYYYCFITLTITIGFDYVALQDQALQTOPOYVAFSFVYILTGLTVIGAFLN 240
 QY 241 LVVLRFTMTNABDEKRAEHRALLTRNGQAGGGGGGSAHTTDTASTAAAGGGGFRNVY 300
 DB 241 LVVLRFTMTNABDEKRAEHRALLTRNGQAGGGGGGSAHTTDTASTAAAGGGGFRNVY 300
 QY 301 AEVLHFQSMCSCLYKRSREKLOYSPMIIPRLDLSDTCTVEQSHSPGCGGRYSDTPSRR 360
 DB 301 AEVLHFQSMCSCLYKRSREKLOYSPMIIPRLDLSDTCTVEQSHSPGCGGRYSDTPSRR 360
 QY 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
 DB 361 CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 4
 ADI27924
 ID ADI27924 standard; protein; 394 AA.
 XX
 AC ADI27924;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human protein #2.
 XX
 KW Human; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease;
 KW Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder;
 KW cardiovascular disorder; cytostatic; neuroprotective; nootropic;
 KW antiparkinsonian; hepatotropic; cardiovascular.
 XX Homo sapiens.
 PN US2003165891-A1.
 PD 04-SEP-2003.
 XX
 PF 15-MAY-2002; 2002US-00146733.
 PR 29-FEB-2000; 2000US-00515520.
 PR 29-FEB-2000; 2000US-0185938P.
 PR 03-MAR-2000; 2000US-00518866.
 PR 07-APR-2000; 2000US-0195734P.
 PR 11-APR-2000; 2000US-0195993P.
 PR 26-APR-2000; 2000US-0199799P.
 PR 19-SEP-2000; 2000US-0233537P.
 PR 25-SEP-2000; 2000US-0235018P.
 PR 25-SEP-2000; 2000US-0235059P.
 PR 15-DEC-2000; 2000US-0256240P.
 PR 18-DEC-2000; 2000US-0256588P.
 PR 21-DEC-2000; 2000US-0258028P.
 PR 28-FEB-2001; 2001US-00796720.
 PR 06-APR-2001; 2001US-00828035.
 PR 11-APR-2001; 2001US-00833081.
 PR 25-APR-2001; 2001US-00843128.
 PR 19-SEP-2001; 2001US-00957683.
 PR 25-SEP-2001; 2001US-00964252.
 PR 25-SEP-2001; 2001US-00964256.
 PR 17-DEC-2001; 2001US-00024623.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Curtis RAJ, Glucksmann MA, Silos-Santiago I;
 PI WPI; 2004-069000/07.
 XX
 DR TWIK-6, TWIK-7, IC29927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9,
 PT alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for

PT preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and
PT cardiovascular disorders.

XX Disclosure; SEQ ID NO 17; 638pp; English.

XX The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,
CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel
CC family (ICF) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927,
CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
CC 53763 ICF nucleic acids and proteins may be used for preventing,
CC diagnosing and treating ICF-related diseases. The sequences may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC ICF proteins by expressing inactive proteins or to supplement the
CC patients own production of ICF proteins. The proteins may also be used as
CC antigens in the production of antibodies against ICF proteins and in
CC assays to identify modulators of ICF protein expression and activity. The
CC anti-ICF protein antibodies, agonists and antagonists may be used to
CC regulate ICF protein expression and activity. The antibodies may also be
CC used as diagnostic agents for detecting the presence of ICF proteins in
CC samples (e.g. by immunoassay). The nucleic acids and proteins may be used
CC to prevent, diagnose and treat a wide variety of disorders, e.g. cancers
CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This
CC sequence represents a human protein used in the scope of the invention.
CC Note: The sequence data for this patent is also available in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 394 AA;

Query Match 100.0%; Score 2042; DB 8; Length 394;
Best Local Similarity 100.0%; Pred. No. 5.3e-213;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRQVRLTALIVCTFTYLLVGAAVFDALSEPELIERQRLRQOELRARNYLSQGGYE 60
Db 1 MKRQVRLTALIVCTFTYLLVGAAVFDALSEPELIERQRLRQOELRARNYLSQGGYE 60
QY 61 ELERVVLRLKPKHAGVQWRFAGSFYFALTITTCYGHAAPESTDGKVCFCFYALLGIPL 120
Db 61 ELERVVLRLKPKHAGVQWRFAGSFYFALTITTCYGHAAPESTDGKVCFCFYALLGIPL 120
QY 121 TLVVFQSLGERINTLVRYLLHRAKGLMRRADVSMANNVLIIGFFSCISTLCIGAAAFSH 180
Db 121 TLVVFQSLGERINTLVRYLLHRAKGLMRRADVSMANNVLIIGFFSCISTLCIGAAAFSH 180
QY 181 YEHWTFFQAYYYCFITLTITIGFDYVALQKQALOTQPYVAFSVYILTGLTVIGAFIN 240
Db 181 YEHWTFFQAYYYCFITLTITIGFDYVALQKQALOTQPYVAFSVYILTGLTVIGAFIN 240
QY 241 LVVLRPMTWNADEKRDABHALLTRNGAGGGGGGSAHTTDTASSTAAGGGGFRNRY 300
Db 241 LVVLRPMTWNADEKRDABHALLTRNGAGGGGGGSAHTTDTASSTAAGGGGFRNRY 300
QY 301 AEVLHFQSCSWLYKSKREKLOYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSPTPSRR 360
Db 301 AEVLHFQSCSWLYKSKREKLOYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSPTPSRR 360
QY 361 CLCSGAPRAISVSTGLHSLSTFRLMKRRSSV 394
Db 361 CLCSGAPRAISVSTGLHSLSTFRLMKRRSSV 394

RESULT 5

AD127925

ID AD127925 standard; protein; 394 AA.

XX AC AD127925;

XX DT 06-MAY-2004 (first entry)

XX DE Human protein #3.

XX

KW

KW

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XX

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Human; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease;
Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder;
cardiovascular disorder; cytostatic; neuroprotective; nootropic;
antiparkinsonian; hepatotropic; cardiovascular.

Homo sapiens.

US2003165891-A1.

04-SEP-2003.

15-MAY-2002; 2002US-00146733.

29-FEB-2000; 2000US-00515520.

29-FEB-2000; 2000US-0185938P.

03-MAR-2000; 2000US-00518866.

07-APR-2000; 2000US-0195734P.

11-APR-2000; 2000US-0195993P.

26-APR-2000; 2000US-0199799P.

19-SEP-2000; 2000US-0233537P.

25-SEP-2000; 2000US-0235018P.

15-DEC-2000; 2000US-0256240P.

18-DEC-2000; 2000US-0256588P.

21-DEC-2000; 2000US-0258028P.

28-FEB-2001; 2001US-00796720.

06-APR-2001; 2001US-00828035.

11-APR-2001; 2001US-00833081.

25-APR-2001; 2001US-00843128.

19-SEP-2001; 2001US-00957683.

25-SEP-2001; 2001US-00964252.

25-SEP-2001; 2001US-00964256.

17-DEC-2001; 2001US-00024623.

(MILL-) MILLENNIUM PHARM INC.

Curtis RAJ, Glucksmann MA, Silos-Santiago I;

WPI; 2004-069000/07.

TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9,
alpha-2delta-4, 54414, or 53763 nucleic acids and proteins, useful for
preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and
cardiovascular disorders.

Disclosure; SEQ ID NO 18; 638pp; English.

The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,
IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel
family (ICF) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927,
TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
53763 ICF nucleic acids and proteins may be used for preventing,
diagnosing and treating ICF-related diseases. The sequences may be used
to treat disorders associated with decreased expression by rectifying
mutations or deletions in a patient's genome that affect the activity of
ICF proteins by expressing inactive proteins or to supplement the
patients own production of ICF proteins. The proteins may also be used as
antigens in the production of antibodies against ICF proteins and in
assays to identify modulators of ICF protein expression and activity. The
anti-ICF protein antibodies, agonists and antagonists may be used to
regulate ICF protein expression and activity. The antibodies may also be
used as diagnostic agents for detecting the presence of ICF proteins in
samples (e.g. by immunoassay). The nucleic acids and proteins may be used
to prevent, diagnose and treat a wide variety of disorders, e.g. cancers
and leukaemia, Alzheimer's disease, Parkinson's disease, multiple
sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This
sequence represents a human protein used in the scope of the invention.
Note: The sequence data for this patent is also available in electronic
format from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 394 AA;

Query Match 100.0%; Score 2042; DB 8; Length 394;

Best Local Similarity 100.0%; Pred. No. 5.3e-213;		Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MKEQNVRLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQQLRARNYLSQGYE	60
Db	1	MKEQNVRLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQQLRARNYLSQGYE	60
QY	61	ELERVVLRKPKHAGVQWRPAGSFYFAITVITTYGHAAPSTDGKVFQVCMFYALLGIPL	120
Db	61	ELERVVLRKPKHAGVQWRPAGSFYFAITVITTYGHAAPSTDGKVFQVCMFYALLGIPL	120
QY	121	TLVMFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFESCISTLCIGAAAFSH	180
Db	121	TLVMFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFESCISTLCIGAAAFSH	180
QY	181	YEHWTFFQAYYYCFITLTITGFDVVALQDQALQTPQVAFSFVYILTGLTVIGAFNL	240
Db	181	YEHWTFFQAYYYCFITLTITGFDVVALQDQALQTPQVAFSFVYILTGLTVIGAFNL	240
QY	241	LVLRFMTWNAEDEKRAHRLLRNGQAGGGGSAHTTDTASSTAAAGGGGFRNVY	300
Db	241	LVLRFMTWNAEDEKRAHRLLRNGQAGGGGSAHTTDTASSTAAAGGGGFRNVY	300
QY	301	AEVLHFQSMCSCWYKSRKLOYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSDTPSRR	360
Db	301	AEVLHFQSMCSCWYKSRKLOYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSDTPSRR	360
QY	361	CLCAGAPRSAISSVSTGLHSLSTFRGLMKRRSSV	394
Db	361	CLCAGAPRSAISSVSTGLHSLSTFRGLMKRRSSV	394
RESULT 6			
AD127915			
ID	AD127915 standard; protein; 395 AA.		
XX	AC AD127915;		
XX	06-MAY-2004 (first entry)		
DT	Human protein #1.		
DE	Human; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease;		
XX	KW Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder;		
KW	cardiovascular disorder; cystostatic; neuroprotective; nootropic;		
KW	anti-parkinsonian; hepatotropic; cardiovascular.		
XX	Homo sapiens.		
OS	US2003165891-A1.		
PN	04-SEP-2003.		
PD	15-MAY-2002; 2002US-00146733.		
XX	29-FEB-2000; 2000US-00515520.		
PR	29-FEB-2000; 2000US-0185938P.		
PR	03-MAR-2000; 2000US-00518866.		
PR	07-APR-2000; 2000US-0195734P.		
PR	11-APR-2000; 2000US-0195993P.		
PR	26-APR-2000; 2000US-0199799P.		
PR	19-SEP-2000; 2000US-0233537P.		
PR	25-SEP-2000; 2000US-0235018P.		
PR	25-SEP-2000; 2000US-0235059P.		
PR	18-DEC-2000; 2000US-0256240P.		
PR	21-DEC-2000; 2000US-0256588P.		
PR	28-FEB-2001; 2001US-00796720.		
PR	06-APR-2001; 2001US-00828035.		
PR	11-APR-2001; 2001US-00833081.		
PR	25-APR-2001; 2001US-00843128.		
PR	19-SEP-2001; 2001US-00957683.		
PR	25-SEP-2001; 2001US-00964252.		

PR	25-SEP-2001; 2001US-00964256.		
XX	17-DEC-2001; 2001US-00024623.		
PA	(MILL-) MILLENNIUM PHARM INC.		
PI	Curtis RAJ, Glucksmann MA, Silos-Santiago I;		
XX	WPI; 2004-0690000/07.		
XX	TIWK-6, TIWK-7, IC23927, TIWK-8, IC47611, IC47615, HNMDA-1, TIWK-9,		
PT	alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for		
PT	preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and		
PT	cardiovascular disorders.		
XX	Disclosure; SEQ ID NO 8; 638pp; English.		
PS	The invention relates to TIWK-5, TIWK-7, IC23927, TIWK-8, IC47611,		
XX	IC47615, HNMDA-1, TIWK-9, alpha-2delta-4, 54414 and 53763 ion channel		
CC	family (ICF) nucleic acids and proteins. The TIWK-6, TIWK-7, IC23927,		
CC	TIWK-8, IC47611, IC47615, HNMDA-1, TIWK-9, alpha-2delta-4, 54414 and		
CC	53763 ICF nucleic acids and proteins may be used for preventing,		
CC	diagnosing and treating ICF-related diseases. The sequences may be used		
CC	to treat disorders associated with decreased expression by rectifying		
CC	mutations or deletions in a patient's genome that affect the activity of		
CC	ICF proteins by expressing inactive proteins or to supplement the		
CC	patients own production of ICF proteins. The proteins may also be used as		
CC	antigens in the production of antibodies against ICF proteins and in		
CC	assays to identify modulators of ICF protein expression and activity. The		
CC	anti-ICF protein antibodies, agonists and antagonists may be used to		
CC	regulate ICF protein expression and activity. The antibodies may also be		
CC	used as diagnostic agents for detecting the presence of ICF proteins in		
CC	samples (e.g. by immunoassay). The nucleic acids and proteins may be used		
CC	to prevent, diagnose and treat a wide variety of disorders, e.g. cancers		
CC	and leukaemia, Alzheimer's disease, Parkinson's disease, multiple		
CC	sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This		
CC	sequence represents a human protein used in the scope of the invention.		
CC	Note: The sequence data for this patent is also available in electronic		
CC	format from USPTO at seqdata.uspto.gov/sequence.html.		
XX	Sequence 395 AA;		
SQ	Query Match 100.0%; Score 2042; DB 8; Length 395;		
	Best Local Similarity 100.0%; Pred. No. 5.3e-213;		
	Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	MKEQNVRLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQQLRARNYLSQGYE	60
Db	2	MKEQNVRLALIVCTFTYLLVGAAVFDALSEPELIERQRLRQQLRARNYLSQGYE	61
QY	61	ELERVVLRKPKHAGVQWRPAGSFYFAITVITTYGHAAPSTDGKVFQVCMFYALLGIPL	120
Db	62	ELERVVLRKPKHAGVQWRPAGSFYFAITVITTYGHAAPSTDGKVFQVCMFYALLGIPL	121
QY	121	TLVMFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFESCISTLCIGAAAFSH	180
Db	122	TLVMFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFESCISTLCIGAAAFSH	181
QY	181	YEHWTFFQAYYYCFITLTITGFDVVALQDQALQTPQVAFSFVYILTGLTVIGAFNL	240
Db	182	YEHWTFFQAYYYCFITLTITGFDVVALQDQALQTPQVAFSFVYILTGLTVIGAFNL	241
QY	241	LVLRFMTWNAEDEKRAHRLLRNGQAGGGGSAHTTDTASSTAAAGGGGFRNVY	300
Db	242	LVLRFMTWNAEDEKRAHRLLRNGQAGGGGSAHTTDTASSTAAAGGGGFRNVY	301
QY	301	AEVLHFQSMCSCWYKSRKLOYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSDTPSRR	360
Db	302	AEVLHFQSMCSCWYKSRKLOYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSDTPSRR	361
QY	361	CLCAGAPRSAISSVSTGLHSLSTFRGLMKRRSSV	394
Db	362	CLCAGAPRSAISSVSTGLHSLSTFRGLMKRRSSV	395

RESULT 7
ADI27916
ID ADI27916 standard; protein; 412 AA.
XX
AC ADI27916;
XX
DT 06-MAY-2004 (first entry)
XX
DE Rat protein #1.
XX
KW Rat; ion channel family; ICF; cancer; leukaemia; Alzheimer's disease;
KW Parkinson's disease; multiple sclerosis; epilepsy; hepatic disorder;
KW cardiovascular disorder; cytostatic; neuroprotective; nootropic;
KW antiparkinsonian; hepatotropic; cardiovascular.
XX
OS Rattus norvegicus.
XX
PN US2003165891-A1.
XX
PD 04-SEP-2003.
XX
PF 15-MAY-2002; 2002US-00146733.
XX
PR 29-FEB-2000; 2000US-00515520.
PR 29-FEB-2000; 2000US-0185938P.
PR 03-MAR-2000; 2000US-00518866.
PR 07-APR-2000; 2000US-0195734P.
PR 11-APR-2000; 2000US-0195993P.
PR 26-APR-2000; 2000US-0199799P.
PR 19-SEP-2000; 2000US-0233537P.
PR 25-SEP-2000; 2000US-0235018P.
PR 25-SEP-2000; 2000US-0235059P.
PR 18-DEC-2000; 2000US-0256240P.
PR 21-DEC-2000; 2000US-0256588P.
PR 28-FEB-2001; 2001US-00796720.
PR 06-APR-2001; 2001US-00828035.
PR 11-APR-2001; 2001US-00833081.
PR 25-APR-2001; 2001US-00843128.
PR 19-SEP-2001; 2001US-00957683.
PR 25-SEP-2001; 2001US-00964252.
PR 25-SEP-2001; 2001US-00964256.
PR 17-DEC-2001; 2001US-00024623.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Curtis RAJ, Glucksmann MA, Silos-Santiago I;
XX
XX WPI; 2004-069000/07.
XX
XX TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9,
PT alpha2delta-4, 54414, or 53763 nucleic acids and proteins, useful for
PT preventing, diagnosing and treating e.g. cancers, Alzheimer's disease and
PT cardiovascular disorders.
XX
XX Disclosure; SEQ ID NO 9; 638pp; English.
XX
XX The invention relates to TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611,
CC IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and 53763 ion channel
CC family (ICF) nucleic acids and proteins. The TWIK-6, TWIK-7, IC23927,
CC TWIK-8, IC47611, IC47615, HNMDA-1, TWIK-9, alpha-2delta-4, 54414 and
CC 53763 ICF nucleic acids and proteins may be used for preventing,
CC diagnosing and treating ICF-related diseases. The sequences may be used
CC to treat disorders associated with decreased expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC ICF proteins by expressing inactive proteins or to supplement the
CC patients own production of ICF proteins. The proteins may also be used as
CC antigens in the production of antibodies against ICF proteins and in
CC assays to identify modulators of ICF protein expression and activity. The
CC anti-ICF protein antibodies, agonists and antagonists may be used to
CC regulate ICF protein expression and activity. The antibodies may also be
CC used as diagnostic agents for detecting the presence of ICF proteins in

CC samples (e.g. by immunoassay). The nucleic acids and proteins may be used
CC to prevent, diagnose and treat a wide variety of disorders, e.g. cancers
CC and leukaemia, Alzheimer's disease, Parkinson's disease, multiple
CC sclerosis, epilepsy, hepatic disorders and cardiovascular disorders. This
CC sequence represents a rat protein used in the scope of the invention.
CC Note: The sequence data for this patent is also available in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 412 AA;

Query Match 90.6%; Score 1850.5; DB 8; Length 412;
Best Local Similarity 88.3%; Pred. No. 4.1e-192;
Matches 363; Conservative 8; Mismatches 23; Indels 17; Gaps 2;
Qy 1 MKRQVRLALIVCTFTYLLVGAADFALDESEPELIERQRLERQLELRARYNLSOGGYE 60
Db 2 MKRQVRLALIVCTFTYLLVGAADFALDESEPELIERQRLERQLELRARYNLSOGGYE 61
Qy 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAPESTDGKVFYFALLGIPL 120
Db 62 ELERVVLRKPKHAGVQWRPAGSFYFAITVTTTIGYGHAAPESTDGKVFYFALLGIPL 121
Qy 121 TLVNFQSLGERINTLVYLLHRAKGLGMRPADVSMANVLI GFSCISTLCIGNAAFSH 180
Db 122 TLVNFQSLGERINTLVYLLHRAKGLGMRHABVSMANVLI GFVSCISTLCIGNAAFSY 181
Qy 181 YEHWTFFQAYYYCFTLTITIGFDYVALQKQALQTOQYVAFSFVYLTGLTVIGAFNL 240
Db 182 YEHWTFFQAYYYCFTLTITIGFDYVALQKQALQTOQYVAFSFVYLTGLTVIGAFNL 241
Qy 241 LVVLRFTMNAEDEKRAEHRALLTRNGQAGGGGG-----GSAHTTTTASSTAAA- 291
Db 242 LVVLRFTMNAEDEKRAEHRALLTRNGQAGGGGG-----GSAHTTTTASSTAAA- 301
Qy 292 -----GGGGRNVVAVLVHFSQSMCSCLWYKREKLOYIPMIIPDLSTSDTCVQS 343
Db 302 GMGVGVGVGGGGRNVVAVLVHFSQSMCSCLWYKREKLOYIPMIIPDLSTSDTCVQS 361
Qy 344 HSSPGGGGRYSDTPSRRLCSGAPRSATSSVSTGLHSLSTPRGLMKRRSSV 394
Db 362 HSSPGGGGRYSDTPSHPCLSGTQRTSAISSVSTGLHSLATPRGLMKRRSSV 412

RESULT 8
AAV95230
ID AAV95230 standard; protein; 405 AA.
XX
AC AAV95230;
XX
DT 29-AUG-2000 (first entry)
XX
DE Mouse potassium channel TASK.
XX
KW TASK; TWIK-related acid-sensitive K+ channel; mouse; potassium channel;
KW drug screening; hypertension; hypotensive; epilepsy; arrhythmia;
KW vascular diseases; neurodegenerative disease; ischaemia; anoxia;
KW endocrine disease; muscle disease; therapy.
XX
OS Mus musculus.
XX
XX Key 50 Location/Qualifiers
FH Modified-site /note= "N-glycosylated"
FT Modified-site 334 /note= "O-phosphorylated"
FT Modified-site 403 /note= "O-phosphorylated"
FT Modified-site 404 /note= "O-phosphorylated"
XX
XX WO200027871-A2.
XX
PD 18-MAY-2000.

XX 09-NOV-1999; 99NO-ID001886.
XX 09-NOV-1998; 98US-0107692P.
XX 08-NOV-1999; 99US-00436265.
XX (CNRS) CNRS CENT NAT RECH SCI.
XX Duprat F, Lesage F, Lazdunski M;
XX WPI; 2000-376487/32.
XX New nucleic acid encoding a non-inactivating outwardly rectifying
PT potassium transport channel, designated TASK2, useful in the treatment of
PT hypertension or dysfunctions of the kidney, liver or pancreas.
XX Disclosure; Fig 8; 91pp; English.
XX The present sequence is that of murine TASK (TWIK-related acid-sensitive
CC K+ channel), a member of a new family of 2P domain potassium channels,
CC also including human TWIK-1 (see AAY79673), human TASK1 (see AAY79674)
CC and novel human TASK2 (see AAY79675). Human and mouse TASK proteins share
CC 85% identity, indicating that they are products of orthologue genes. Host
CC cells expressing TWIK-1 family members can be used to screen for
CC substances that modulate the activity of members of the TWIK-1 family of
CC potassium channels. The drugs identified may be useful in the treatment
CC of diseases of the heart or of the nervous system, such as epilepsy,
CC arrhythmia, vascular diseases, neurodegenerative diseases, kidney, liver
CC or pancreas diseases, hypertension, diseases associated with ischaemia or
CC anoxia, endocrine diseases associated with anomalies of hormone
CC secretion, and muscle diseases
XX Sequence 405 AA;
Query Match 89.1%; Score 1819; DB 3; Length 405;
Best Local Similarity 88.1%; Pred. No. 1.1e-188;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;
QY 4 QNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARNLNSGGYEEL 63
Db 1 ENVRTLALIVCTFTYLLVGAADFDALESEPEMERQRLRQELRARNLNSGGYEEL 60
QY 64 RVVRLKPKHAGVQWRFAAGSFYFAITVTTIGYGHAAAPSTDGKVFCEMFIALLGIPLTIV 123
Db 61 RVVRLKPKHAGVQWRFAAGSFYFAITVTTIGYGHAAAPSTDGKVFCEMFIALLGIPLTIV 120
QY 124 MFQSLGERINTLVRYLLHRAKGLGMRADVSMMANNVLIGFVSCISTLCIGAAAFSHYEH 183
Db 121 MFQSLGERINTLVRYLLHRAKGLGMRADVSMMANNVLIGFVSCISTLCIGAAAFSHYER 180
QY 184 WTFPQAYYYCFITLTTIGFDYVALQKQALQTPQYVAFSFYVILTGLTVIGAFNLV 243
Db 181 WTFPQAYYYCFITLTTIGFDYVALQKQALQTPQYVAFSFYVILTGLTVIGAFNLV 240
QY 244 LRFMTWNAEDEKRAEHRALLTHNGQAVGLGSLCISLGSIGDVRPDPVTCAAAAGGVG 291
Db 241 LRFMTWNAEDEKRAEHRALLTHNGQAVGLGSLCISLGSIGDVRPDPVTCAAAAGGVG 300
QY 292 --GGGGFRNVAEVLHFSQMCCLWYKREKLOYSTIPMLIPDLSTSDTCVESHSSPGG 349
Db 301 GVGGSFRNVAEVLHFSQMCCLWYKREKLOYSTIPMLIPDLSTSDTCVESHSSPGG 360
QY 350 GGRYSTPTPARRCICSGAPRSASSVSTGLHSLSTFRLMKRRSSV 394
Db 361 GGRYSTPTPARRCICSGAPRSASSVSTGLHSLSTFRLMKRRSSV 405
RESULT 9
AAU07620
ID AAU07620 standard; protein; 309 AA.
XX
AC AAU07620;
XX

DT 21-NOV-2001 (first entry)
XX Mouse 2P channel protein #1.
XX Transmembrane potassium ion channel protein; inward potassium flux;
KW pest control; membrane potential; pesticide; antihelminthic; nematode;
KW insect; 2P channel; mouse.
XX Mus musculus.
XX WO200161006-A2.
XX 23-AUG-2001.
XX 14-FEB-2001; 2001WO-US004680.
XX 15-FEB-2000; 2000US-00503849.
XX (BADI) BASF CORP.
XX Pausch MH;
XX WPI; 2001-536570/59.
XX N-PSDB; AAS12179.
XX New polypeptide, a mutant potassium ion channel protein for improving
PT inward potassium flux under acidic conditions.
XX Example 18; Page 53; 131pp; English.
XX The invention relates to a mutant potassium ion channel protein, having
CC four membrane spanning domains and two pore forming domains, comprising a
CC mutation at the second pore forming domain. The expression of the mutant
CC protein in a cell confers improved inward potassium flux and the ability
CC to grow in the presence of potassium. Mutant proteins and their
CC corresponding polynucleotide sequences can therefore be used to improve
CC inward potassium flux into cells under acidic conditions by modulating
CC the membrane potential using therapeutic agents. The sequences may be
CC used to develop agonists and antagonists of potassium channel proteins in
CC order to control pests such as nematodes and insects. This sequence
CC represents a mouse 2P channel protein
XX Sequence 309 AA;
Query Match 60.5%; Score 1235.5; DB 4; Length 309;
Best Local Similarity 83.9%; Pred. No. 2.6e-125;
Matches 250; Conservative 8; Mismatches 27; Indels 13; Gaps 3;
QY 4 QNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARNLNSGGYEEL 63
Db 13 ENVRTLALIVCTFTYLLVGAADFDALESEPEMERQRLRQELRARNLNSGGYEEL 72
QY 64 RVVRLKPKHAGVQWRFAAGSFYFAITVTTIGYGHAAAPSTDGKVFCEMFIALLGIPLTIV 123
Db 73 RVVRLKPKHAGVQWRFAAGSFYFAITVTTIGYGHAAAPSTDGKVFCEMFIALLGIPLTIV 132
QY 124 MFQSLGERINTLVRYLLHRAKGLGMRADVSMMANNVLIGFVSCISTLCIGAAAFSHYEH 183
Db 133 MFQSLGERINTLVRYLLHRAKGLGMRADVSMMANNVLIGFVSCISTLCIGAAAFSHYER 192
QY 184 WTFPQAYYYCFITLTTIGFDYVALQKQALQTPQYVAFSFYVILTGLTVIGAFNL 241
Db 193 WTFPQAYYYCFITLTTIGFDYVALQKQALQTPQYVAFSFYVILTGLTVIGAFNL 249
QY 242 VVLRFTWNAEDEKRAEHRALLTHNGQAVGLGSLCISLGSIGDVRPDPVTCAAA 291
Db 250 VVLRFTWNAEDEKRAEHRALLTHNGQAVGLGSLCISLGSIGDVRPDPVTCAAA 307
RESULT 10
AAB18807
ID AAB18807 standard; protein; 374 AA.
XX

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AC AAB18807;
XX
DT 22-JAN-2001 (first entry)
XX
DE Amino acid sequence of a human DKN1 polypeptide.
XX
KW Human; DKN1; potassium channel; cancer; pulmonary disease; depression;
KW cardiovascular disease; inflammatory disease; renal disease; pain;
KW psychiatric disorder; schizophrenia; neurodegenerative disease;
KW Alzheimer's disease; neurological disorder; migraine; epilepsy;
KW sleep-related disorder; erectile dysfunction; alopecia.
XX
OS Homo sapiens.
XX
FN WO200053628-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-EP001750.
XX
PR 05-MAR-1999; 99GB-00005061.
PR 10-FEB-2000; 2000GB-00003112.
XX
PA (SMIK ) SMITHLINE BEECHAM PLC.
XX
PI Duckworth DM, Godden RJ, Chapman CG, Meadows HJ;
XX
DR WPI; 2000-587424/55.
XX
DR N-PSDB; AAA75886.
XX
PT Polypeptides and polynucleotides of the potassium channel family, useful
PT for identifying agonists/antagonists of therapeutic use and diagnosis and
PT treatment of cancer, pulmonary, cardiovascular, inflammatory and renal
PT disease.
XX
PS Claim 1; Page 25; 36pp; English.
XX
CC The present sequence represents human DKN1 polypeptide. The polypeptide
CC is a member of the potassium channel family. The DKN1 polypeptides and
CC polynucleotides are useful for treating diseases including cancer,
CC pulmonary, cardiovascular, inflammatory or renal diseases, pain,
CC psychiatric disorders including depression and schizophrenia,
CC neurodegenerative disease including Alzheimer's, neurological disorders,
CC migraine, epilepsy, sleep-related disorders, erectile dysfunction and
CC alopecia. DKN1 polynucleotides are useful as diagnostic reagents for
CC detecting mutations in the associated gene
XX
SQ Sequence 374 AA;

Query Match 54.7%; Score 1116; DB 3; Length 374;
Best Local Similarity 59.0%; Pred. No. 3.5e-112;
Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

QY 1 MKRQVRLALIVCTFTYLLVGAADFALDSEPELIERQRLRQOELRARNLSQGGYE 60
DB 1 MKRQVRLSLIVCTFTYLLVGAADFALDSEPELIERQRLRQOELRARNLSQGGYE 60
QY 61 ELERVRLKPKHAGVQWRFGSFYFAITVITIGYHAAFPSTGGKVFCEMFYALLGIPL 120
DB 61 QLELVILQSEPHRAGVQWRFGSFYFAITVITIGYHAAFPSTGGKVFCEMFYALLGIPL 120
QY 121 TLVMEFQSLGERINTLVRLHRAKGLGMRADVSMANNVLGFFPSCISTLCIGAAAFSH 180
DB 121 TLVMEFQSLGERNMTFRYLLRLKIKCCGNRNTDVSMNNVTGVFFSCMTLCIGAAAFSQ 180
QY 181 YEHWTFQAYYYCFITLTITIGFDYVALQDALQTPQYAFSFYILTLGTIVGAFLN 240
DB 181 CEWSFFHAYYYCFITLTITIGFDYVALQTKGALQKPLVAFSFYILVGLTVIGAFLN 240
QY 241 LVVLRPMTVADEKRDHRAHLLTFNGOAGGGGGGSAHTTDTASSTAAGGGGFRNRY 300
DB 241 LVVLRFLTNSEDRDRAERASL-----AGNRNSMWIHIPEEPRPS-----RPRY 286

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QY 301 -AEVLHFQSMGSCILWYKSRKLOYSIPMIIPDLSTSDTCVEQSHSPGGGRYSDTFPSR 359
DB 287 KADVPDLQSVCTCYRSQD---YGRSVAQNSFSAKLAPHYFHSISYKIEISPSLTK 343
QY 360 RCLCGAPRSASISVSGLHLSLSTFRGLMKRRSSV 394
DB 344 NSLFP-----SPISSISPLHSGFTDQRLMKRRKSV 374

RESULT 11
AAB18813
ID AAB18813 standard; protein; 374 AA.
AC AAB18813;
XX
DT 22-JAN-2001 (first entry)
XX
DE Protein encoded by an EST related to a human DKN1 cDNA.
XX
KW Human; DKN1; potassium channel; cancer; pulmonary disease; depression;
KW cardiovascular disease; inflammatory disease; renal disease; pain;
KW psychiatric disorder; schizophrenia; neurodegenerative disease;
KW Alzheimer's disease; neurological disorder; migraine; epilepsy;
KW sleep-related disorder; erectile dysfunction; alopecia;
KW expressed sequence tag; EST.
XX
OS Homo sapiens.
XX
FN WO200053628-A2.
XX
PD 14-SEP-2000.
XX
PF 02-MAR-2000; 2000WO-EP001750.
XX
PR 05-MAR-1999; 99GB-00005061.
PR 10-FEB-2000; 2000GB-00003112.
XX
PA (SMIK ) SMITHLINE BEECHAM PLC.
XX
PI Duckworth DM, Godden RJ, Chapman CG, Meadows HJ;
XX
DR WPI; 2000-587424/55.
XX
DR N-PSDB; AAA75887.
XX
PT Polypeptides and polynucleotides of the potassium channel family, useful
PT for identifying agonists/antagonists of therapeutic use and diagnosis and
PT treatment of cancer, pulmonary, cardiovascular, inflammatory and renal
PT disease.
XX
PS Claim 12; Page 26; 36pp; English.
XX
CC The present sequence is encoded by an expressed sequence tag (EST) which
CC is related to a cDNA encoding a human DKN1 polypeptide. The polypeptide
CC is a member of the potassium channel family. The DKN1 polypeptides and
CC polynucleotides are useful for treating diseases including cancer,
CC pulmonary, cardiovascular, inflammatory or renal diseases, pain,
CC psychiatric disorders including depression and schizophrenia,
CC neurodegenerative disease including Alzheimer's, neurological disorders,
CC migraine, epilepsy, sleep-related disorders, erectile dysfunction and
CC alopecia. DKN1 polynucleotides are useful as diagnostic reagents for
CC detecting mutations in the associated gene
XX
SQ Sequence 374 AA;

Query Match 54.7%; Score 1116; DB 3; Length 374;
Best Local Similarity 59.0%; Pred. No. 3.5e-112;
Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

QY 1 MKRQVRLALIVCTFTYLLVGAADFALDSEPELIERQRLRQOELRARNLSQGGYE 60
DB 1 MKRQVRLSLIVCTFTYLLVGAADFALDSEPELIERQRLRQOELRARNLSQGGYE 60
QY 61 ELERVRLKPKHAGVQWRFGSFYFAITVITIGYHAAFPSTGGKVFCEMFYALLGIPL 120

```

Db 61 QLELVILQSEPHRAGVQWKFAAGSYFAITVITTTIGYHAAAPGTDAGKAFCMFYAVLGIPL 120
QY 121 TLVMFQSLGERINTLVYLLHRAKKGKGLMRRADYSMANMVLIGFPSCISTLCIGAAAFSH 180
Db 121 TLVMFQSLGERMNTFVYLLKRIKCCGMRTDVS MENMVTGFFSCMGTLCIGAAAFSQ 180
QY 181 YEHWTFFQAYYYCITITTTIGFGDYVALQKQALQTOPOQVAFSVFVYLLTGLTVIGAFNL 240
Db 181 CEWSFFHAYYYCITITTTIGFGDYVALQKQALQKPLVAFSFMVILVGLTVIGAFNL 240
QY 241 LVLRFMTWNAEDKRAEHRALITRNGAGGGGGGSAHTTDTASTAAGGGGFRNVY 300
Db 241 LVLRFMTWNSDEDRDAERASL-----AGNRNSMVIHIPERPRPS-----RPRY 286
QY 301 -AEVLHFQSMCCLWYKSRKLYSPIMIPRDLSTSDTCVEQSHSPGGGGRYSDTPSR 359
Db 287 KADVPDLQSVCTCYRSQD---YGRSVAPQNSFAKLAPHYFHSYKIEISPTLK 343
QY 360 RCLCSGAPRAISVSTGLHSLSTFRGLMKRRSSV 394
Db 344 NSLFP-----SPISSISPLHSFTDHQRLMKRRKSV 374

RESULT 12

AAG63938

ID AAG63938 standard; protein; 374 AA.

XX AC AAG63938;

XX DT 29-OCT-2001 (first entry)

XX DE Amino acid sequence of human potassium channel protein KCNB.

XX KW Human; potassium channel protein; KCNB; breast tissue; cancer; stroke;

XX KW potassium channel-associated disorder; brain associated disorder;

XX KW epilepsy; Alzheimer's disease; Parkinson's disease; multiple sclerosis;

XX KW migraine; psychiatric disorder; depression; schizophrenia; diabetes;

XX KW bipolar disease; heart disease; arrhythmia; pancreas disease;

XX KW pancreatitis.

XX OS Homo sapiens.

XX WO200166741-A2.

XX 13-SEP-2001.

XX PF 02-MAR-2001; 2001WO-US006801.

XX PR 03-MAR-2000; 2000US-0186915P.

XX PA (TULA-) TULARIK INC.

XX PI Mu D, Powers S;

XX WPI; 2001-522949/57.

XX DR N-PSDB; AAH74999.

XX A nucleic acid encoding a potassium channel, termed KCNB (potassium

channel expressed in breast), useful in the diagnosis, prognosis or

treatment of diseases associated with altered KCNB activity or

expression, e.g. cancer and diabetes.

XX Claim 16; Page 79; 82pp; English.

XX The present sequence represents a human potassium channel protein, termed

KCNB. KCNB is expressed in breast tissue. The KCNB polypeptides are

useful for identifying a compound that modulates its activity. The KCNB

polypeptide and nucleic acid are useful for detecting cancer cells in

biological samples. The inhibitor of the potassium channel polypeptide is

useful for inhibiting proliferation of a cancer cell and for treating a

potassium channel-associated disorder. The KCNB nucleic acids, proteins,

and/or antibodies are useful in the diagnosis or prognosis, or treatment

CC of diseases associated with altered KCNB activity or expression. Such
CC diseases are cancer, brain associated disorders (such as epilepsy,
CC Alzheimer's disease, Parkinson's disease, stroke, multiple sclerosis,
CC migraine), psychiatric disorders (such as depression, schizophrenia,
CC bipolar disease) and diseases related to the heart (such as
CC arrhythmias), diseases related to pancreas (such as pancreatitis and
CC diabetes)

XX SQ Sequence 374 AA;

Query Match 54.7%; Score 1116; DB 4; Length 374;

Best Local Similarity 59.0%; Pred. No. 3.5e-112;

Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

QY 1 MKQNVRTALIVCTTLYLLVGAAVFDALSEPELIERORLELRQBELRARNYLSQGGYE 60

Db 1 MKQNVRTLSLVCTTLYLLVGAAVFDALSEDEHEEELKAEETRIKKNYISSDYR 60

QY 61 ELERVVLRKPKHAGVQWKPAGSYFAITVITTTIGYHAAAPSTDGKVKFCMFAVLLGIPL 120

Db 61 QLELVILQSEPHRAGVQWKFAAGSYFAITVITTTIGYHAAAPGTDAGKAFCMFYAVLGIPL 120

QY 121 TLVMFQSLGERINTLVYLLHRAKKGKGLMRRADYSMANMVLIGFPSCISTLCIGAAAFSH 180

Db 121 TLVMFQSLGERMNTFVYLLKRIKCCGMRTDVS MENMVTGFFSCMGTLCIGAAAFSQ 180

QY 181 YEHWTFFQAYYYCITITTTIGFGDYVALQKQALQTOPOQVAFSVFVYLLTGLTVIGAFNL 240

Db 181 CEWSFFHAYYYCITITTTIGFGDYVALQKQALQKPLVAFSFMVILVGLTVIGAFNL 240

QY 241 LVLRFMTWNAEDKRAEHRALITRNGAGGGGGGSAHTTDTASTAAGGGGFRNVY 300

Db 241 LVLRFMTWNSDEDRDAERASL-----AGNRNSMVIHIPERPRPS-----RPRY 286

QY 301 -AEVLHFQSMCCLWYKSRKLYSPIMIPRDLSTSDTCVEQSHSPGGGGRYSDTPSR 359

Db 287 KADVPDLQSVCTCYRSQD---YGRSVAPQNSFAKLAPHYFHSYKIEISPTLK 343

QY 360 RCLCSGAPRAISVSTGLHSLSTFRGLMKRRSSV 394

Db 344 NSLFP-----SPISSISPLHSFTDHQRLMKRRKSV 374

RESULT 13

AAE13279

ID AAE13279 standard; protein; 374 AA.

XX AC AAE13279;

XX DT 12-FEB-2002 (first entry)

XX DE Human transporters and ion channels (TRICH)-6.

XX KW Human; transporter and ion channel; TRICH; akinesia; cystic fibrosis;

XX KW diabetes mellitus; Parkinson's disease; myasthenia gravis; dementia;

XX KW cardiac disorder; angina; hypertension; myocarditis; hyperglycaemia;

XX KW neurological disorder; Alzheimer's disease; cataract; infertility;

XX KW Wilson's disease; schizophrenia; Grave's disease; Addison's disease;

XX KW Huntington's disease; multiple sclerosis; meningitis; hypotensive;

XX KW cardiac; noctropic; neuroprotective; neuroleptic; ophthalmological;

XX KW antithyroid; anticonvulsant; goitre; antiinflammatory.

XX OS Homo sapiens.

XX Key Location/Qualifiers.

XX Peptide 1..25

XX Protein /label= Signal_peptide

XX Domain 26..374

XX /note= "Human mature TRICH6 protein"

XX /label= Transmembrane_domain

XX WO200177174-A2.

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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:02:40 ; Search time 20.7368 Seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-09-503-089A-5
Perfect score: 2042
Sequence: 1 MKRQNVRTLALIVCTFTYLL.....STGLHSLSTFRGLMKRRSSV 394
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	846	41.4	330	JC7703	TASK-5 protein - h
2	820	40.2	329	T43509	probable potassium
3	806.5	39.5	336	T32347	outward rectifier
4	599	29.3	334	T19860	hypothetical prote
5	599	29.3	364	T43361	probable potassium
6	320.5	15.7	336	S65566	inward rectifier p
7	307.5	15.1	513	T28933	hypothetical prote
8	293	14.3	393	T25392	hypothetical prote
9	276.5	13.5	1910	H88124	protein T12C9.3 [i
10	275	13.5	524	T23907	hypothetical prote
11	268	13.1	1539	T30037	hypothetical prote
12	262	12.8	443	T21598	hypothetical prote
13	261.5	12.8	1001	T13807	hypothetical prote
14	259.5	12.7	335	S44635	potassium channel
15	258.5	12.7	427	T27681	f22b7.7 protein -
16	258	12.6	383	T23182	hypothetical prote
17	256.5	12.6	452	T21118	hypothetical prote
18	251	12.3	544	T43364	potassium channel
19	251	12.3	576	T43363	potassium channel
20	250	12.2	569	T43531	probable potassium
21	248	12.1	444	T26229	hypothetical prote
22	247.5	12.1	392	T45032	hypothetical prote
23	245	12.0	769	T27550	hypothetical prote
24	244	11.9	381	T43393	potassium channel
25	243	11.9	528	T21834	hypothetical prote
26	239.5	11.7	522	T24265	hypothetical prote
27	235.5	11.5	475	T27725	hypothetical prote
28	234.5	11.5	485	T24201	hypothetical prote
29	231.5	11.3	484	T43529	probable potassium

30	231.5	11.3	519	2	T16629	hypothetical prote
31	229	11.2	325	2	T15584	hypothetical prote
32	229	11.2	461	2	T43394	potassium channel
33	222.5	10.9	600	2	T24626	hypothetical prote
34	216	10.6	350	2	T15178	hypothetical prote
35	215.5	10.6	643	2	T26616	hypothetical prote
36	211	10.3	539	2	T23700	hypothetical prote
37	210.5	10.3	504	2	T22269	hypothetical prote
38	210	10.3	1136	2	T26953	hypothetical prote
39	205.5	10.1	586	2	T21683	hypothetical prote
40	201.5	9.9	551	2	T16426	hypothetical prote
41	201.5	9.9	555	2	T43357	potassium channel
42	200.5	9.8	700	2	T27364	hypothetical prote
43	199.5	9.8	660	2	T21551	hypothetical prote
44	193.5	9.5	523	2	T23373	hypothetical prote
45	190.5	9.3	383	2	T23746	hypothetical prote

ALIGNMENTS

RESULT 1
JC7703
TASK-5 protein - human
C;Species: Homo sapiens (man)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: JC7703
R;Kim, D.; Gnatenco, C.
Biochem. Biophys. Res. Commun. 284, 923-930, 2001
A;Title: TASK-5, a new member of the tandem-pore K+ channel family.
A;Reference number: JC7703; MUID:21303050; PMID:11409881
A;Accession: JC7703
A;Molecule type: DNA
A;Residues: 1-330 <KIM>
A;Cross-references: GB:AL118522
C;Comment: This protein, a new member of the tandem-pore K+ channel family with four tr
hormone secretion, but does not produce a functional plasma membrane K+ current by itse
C;Genetics:
A;Gene: task-5
A;Map position: 20q12
C;Keywords: transmembrane protein
F;7-30/Domain: transmembrane segment #status predicted <TMS1>
F;107-128/Domain: transmembrane segment #status predicted <TMS2>
F;129-155/Region: hydrophobic cytoplasmic linker #status predicted
F;156-180/Domain: transmembrane segment #status predicted <TMS3>
F;220-240/Domain: transmembrane segment #status predicted <TMS4>

Query Match 41.4%; Score 846; DB 2; Length 330;
Best Local Similarity 64.7%; Pred. NO. 1e-68;
Matches 167; Conservative 32; Mismatches 59; Indels 0; Gaps 0;

QY	1	MKRONVRTLALIVCTFTYLLVGAAVFDALSEPELTERORLELRQCELRARYNLSOGGYE	60
DB	1	MRRPSVRAAGLVCTLCYLLVGAAVFDALSEAEGRQLLVQKRALRKFFSADYR	60
QY	61	ELERVVRLKPKAGVQWRFAGSFYFAITVITTYGYHAAPSTDGKVKFCMFYALLGIPL	120
DB	61	ELERLALQAEPRHGRQWKFGSFFYFAITVITTYGYHAAPSTDGKVKFCMFYALLGIPL	120
QY	121	TLVMSQISGERINTLVRYLLHRAKGLGNRRADVSMANVILGFFSCISTLCIGAAAFSH	180
DB	121	TLVTFQSLGERLNAAVVRLLAAKCCGLRWTCVSTENLVAGLLCAATLALGAVAFSH	180
QY	181	YEHWTFFQAYYYCFTLTITTYGDDVVALQDQLOTPQYVAFSPFYVILTLTVIGAFLN	240
DB	181	FGWTFHFFAYYYCFTLTITTYGDDVVALQDQLOTPQYVAFSPFYVILTLTVIGAFLN	240
QY	241	LVVLRFTMTNABDEKRDA	258
DB	241	LVVLRFLVASADWPERAA	258

RESULT 2

R:Gattung, S.; Wu, X.
submitted to the EMBL Data Library, March 1996
A:Description: The sequence of *C. elegans* cosmid F20A1.
A:Reference number: Z20726
A:Accession: T30037
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1539 <GAT>
A:Cross-references: UNIPROT:Q19611; EMBL:U53150; PIDN:AAA96127.1; GSPDB:GN000023; CESP:F20A1
A:Experimental source: strain Bristol N2; clone F20A1
C:Genetics:
A:Map position: 5
A:Introns: 19/3; 41/2; 71/2; 110/3; 135/2; 190/1; 246/1; 287/3; 491/3; 598/2; 983/2; 110/3
Query Match 13.1%; Score 268; DB 2; Length 1539;
Best Local Similarity 24.6%; Pred. No. 1.3e-15;
Matches 96; Conservative 60; Mismatches 126; Indels 108; Gaps 13;
QY 8 TIALIVCTTYLLVGAADFALSEPELIERQ-----RLELQOELRA-RYNLSQGG 58
DB 88 TPKLLIIIGLYSPIGAHIFWYLEVPTDLEAREDFHQRKIAREVMVNLRAIFYNREDR 147
QY 59 YEELERVVLRLKPKHAGVQ-----WRFAGSFYFAITVTTIGYGHAASTDDGKVFCM 111
DB 148 ERWKHAILKFE-EDIGLEPVIETVTFWMSFLYAGTFTTIGYGNIACTRAGQIATM 206
QY 112 FYALLGIPITLVNFOSL-----GERI----- 132
DB 207 VFAVGIPIMLVNLTSLNNFLKWKILITNGVSDMTLYIGVRLGITVIRQDEVOQELRYT 266
QY 133 ----NTLVRVLL--HRAKGLGHRADVSMNM-----VLIGFFSCISTL 171
DB 267 KLAKTMKRWKLSKHGAPSAISNSSENLSTPEDDEBEEIHDQPPVLSLTIAATVAMI 326
QY 172 CIGAAFSHYEHTWTFQAYYCFITLTITGFDYVALQDQALQTOPOQVAVSFVYLNG 231
DB 327 ILSSAAVCLUFEDWTPTPTSPYCFISLTITGLGD-----VTPANPEYMIATFGVVIWG 378
QY 232 LTVIGAFNLVLRFMTMADEKRAEHRALLTRNGQAGGGGGGSAHTTDTASTAA 291
DB 379 LSLMTVICIDVLEKLAQTM-----ALLOKLTEYMEAVKSG-----DPNAAASAMWA 425
QY 292 GGGG-----FRNYAEVL-HFQSMCS 311
DB 426 GFQGRAKFLMPLISKNEGAKVMDKFKQDCS 455
RESULT 12
T21598
hypothetical protein F31D4.7 - *Caenorhabditis elegans*.
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21598
R:Morimore, B.
submitted to the EMBL Data Library, March 1997
A:Reference number: Z19447
A:Accession: T21598
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-443 <WIL>
A:Cross-references: UNIPROT:O45422; EMBL:Z92832; PIDN:CA07375.1; GSPDB:GN000023; CESP:F31D4
A:Experimental source: clone F31D4
C:Genetics:
A:Gene: CESP:F31D4.7
A:Map position: 5
A:Introns: 13/3; 90/2; 149/1; 222/3; 290/3
Query Match 12.8%; Score 262; DB 2; Length 443;
Best Local Similarity 25.0%; Pred. No. 1e-15;
Matches 78; Conservative 55; Mismatches 113; Indels 66; Gaps 9;
QY 11 LIVCTTYLLVGAADFALSE--EPEL-----IERQLELRQOELRAYNLSQ----- 56

DB 17 LIIVFLIYCISGLVFWLIEEYQSELRDAMOHKIENRTARVDAMKKIFNNSDLYIY 76
QY 57 -----GGYEELERVVLRLKPKHAGVQWRPAGSFYFAITVTTIGYGHAA 100
DB 77 KGNTSRLTFTTFIEELGSYEN---QLGVKWSQOKMDWDFWNAVLPAFTICTTIGYGHIV 132
QY 101 PSTDGGKVFCEYALLGIPITLVNFQSLGERINTLVRYLLHRAKGL----- 147
DB 133 PMTDAGRLMTIFALFGIPLMLLVLDQDFGLKLTITMKFPWFQTYKLMRRIMRCCTKQPIE 192
QY 148 -----GMRRADVSMANMVL-IGTFSCISTLCIGAAAFSHYEH-WTFQAYYCFITLTT 199
DB 193 EMKEIERQERHDLDFIDPLPGVIALIVTWIFICSEFVLSVDHNNWTLLESFPPFFTSLSLT 252
QY 200 IGFGDYVALQDQALQTOPOQVAVSFVYLTGLTVIGAFNLVLRFMT---MNADEKR 256
DB 253 VGLGDLV-----PSSPRLLITWFGFILVGLSVLMVINLLOAKMKSTYEAGRNDKXT 304
QY 257 DAHRALLTRNG 268
DB 305 PHIHQTLPTSLG 316
RESULT 13
T13807
potassium channel protein - fruit fly (*Drosophila melanogaster*)
C:Species: *Drosophila melanogaster*
C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13807
R:Goldstein, S.A.; Price, L.A.; Rosenthal, D.N.; Pausch, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 13258-13261, 1996
A:Title: ORK1, a potassium-selective leak channel with two pore domains cloned from *Drosophila*
A:Reference number: Z17770; MUID:97075152; PMID:8917578
A:Accession: T13807
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1001 <GOL>
A:Cross-references: UNIPROT:Q94526; EMBL:U55321; NID:G3808067; PID:G3808068; PIDN:AAC669
C:Genetics:
A:Gene: ORK1
A:Cross-references: FlyBase:FBgn0017561
A:Map position: 1
Query Match 12.8%; Score 261.5; DB 2; Length 1001;
Best Local Similarity 25.0%; Pred. No. 3e-15;
Matches 69; Conservative 65; Mismatches 107; Indels 35; Gaps 8;
QY 7 RTALIVCTTYLLVGAADFALSEPELIERQLELRQOELRAYNLSQGGYEEL----- 62
DB 5 RWILLIIFYISYLMFGAAIYYHIEGEEKIS-----RAEQKQAQIAINEYLLEELGDKN 58
QY 63 ----ERVVLR-----KP-----HKAGVQWRPAGSFYFAITVTTIGYGHAASTDDG 106
DB 59 TTTQDEILQRIISDYCKKPVTLPTDTPYTTFTHAFFAFTVCTGVYGNISPTTFAG 118
QY 107 KVFCEYALLGIPITLVNFQSLGERINTLVRYLLHRAK-----GLGMRRADVSMANMVL 161
DB 119 RMIMIAYSVIGIPVNGILLFAGLGEYFGRTFEAIYRKYKYSTDMHYVPPQLGLITTV 178
QY 162 IGTFSCIST-LCIGAAAFSHYEHWTFFQAYYCFITLTTIGFDYV-ALQKDQALQTOPO 219
DB 179 IALIFGIALFLLPWSVTFYFENWPSYLSLYSYVTTTTTIGFDYVTFGANQPKBFGW 238
QY 220 VYAFSFVLTGLTVIGAFNLVLRFMTMADEK 255
DB 239 FVYQIFVIVFWIFSLGYL--VMIMFITRGLQSKK 272
RESULT 14
S44635
f2b27.7 protein - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:40:02 ; Search time 86.5115 Seconds
(without alignments)
1759.475 Million cell updates/sec

Title: US-09-503-089A-5
Perfect score: 2042
Sequence: 1 MRQNVRTIALIVCTFYLL.....STGLHSLSTFRGLMKRRSSV 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 386332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10F_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2042	100.0	394	9 US-09-939-484-4	Sequence 4, Appli
2	2042	100.0	394	9 US-09-939-483-4	Sequence 4, Appli
3	2042	100.0	394	9 US-09-798-584-15	Sequence 15, Appli
4	2042	100.0	394	14 US-10-146-733-17	Sequence 17, Appl
5	2042	100.0	394	14 US-10-146-733-18	Sequence 18, Appl
6	2042	100.0	395	14 US-10-146-733-8	Sequence 8, Appli
7	1850.5	90.6	412	14 US-10-146-733-9	Sequence 9, Appli
8	1819	89.1	405	9 US-09-939-484-5	Sequence 5, Appli
9	1819	89.1	405	9 US-09-939-483-5	Sequence 5, Appli
10	1278	62.6	258	9 US-09-746-491-61	Sequence 61, Appl
11	1224	59.9	312	8 US-08-816-011-55	Sequence 55, Appl

Query Match 100.0%; Score 2042; DB 9; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.4e-180;

12	1224	59.9	312	17	US-10-870-492-55	Sequence 55, Appl
13	1154	56.5	233	15	US-10-459-190-15	Sequence 15, Appli
14	1116	54.7	374	9	US-09-798-584-1	Sequence 1, Appli
15	1116	54.7	374	14	US-10-146-733-41	Sequence 41, Appli
16	1116	54.7	374	15	US-10-257-022-6	Sequence 6, Appli
17	1116	54.7	374	15	US-10-074-978A-194	Sequence 194, App
18	1077.5	52.8	387	15	US-10-074-978A-195	Sequence 195, App
19	1069.5	52.4	365	9	US-09-746-491-60	Sequence 60, Appl
20	846	41.4	330	9	US-09-746-491-59	Sequence 59, Appl
21	846	41.4	330	15	US-10-173-999-42	Sequence 42, Appl
22	846	41.4	330	15	US-10-074-978A-192	Sequence 192, App
23	846	41.4	330	15	US-10-074-978A-193	Sequence 193, App
24	846	41.4	400	14	US-10-146-733-5	Sequence 5, Appli
25	838	41.0	330	9	US-09-746-491-58	Sequence 58, Appl
26	838	41.0	330	15	US-10-074-978A-191	Sequence 191, App
27	838	41.0	330	15	US-10-336-472-76	Sequence 76, Appl
28	838	41.0	393	9	US-09-746-491-22	Sequence 22, Appl
29	838	41.0	400	14	US-10-146-733-2	Sequence 2, Appli
30	838	41.0	400	15	US-10-257-022-13	Sequence 13, Appl
31	774	37.9	279	9	US-09-864-761-34389	Sequence 34389, A
32	619	30.3	212	15	US-10-074-978A-24	Sequence 24, Appl
33	507.5	24.9	179	15	US-10-424-599-216417	Sequence 216417,
34	370	18.1	370	9	US-09-939-484-8	Sequence 8, Appli
35	370	18.1	370	9	US-09-939-483-8	Sequence 8, Appli
36	369	18.1	411	9	US-09-828-746-6	Sequence 6, Appli
37	366.5	17.9	295	16	US-10-343-903-8	Sequence 8, Appli
38	366	17.9	487	17	US-10-461-862-129	Sequence 129, App
39	364	17.8	422	16	US-10-349-528-20	Sequence 20, Appl
40	364	17.8	426	8	US-08-816-011-45	Sequence 45, Appl
41	364	17.8	426	17	US-10-870-492-45	Sequence 45, Appl
42	363	17.8	411	9	US-09-828-746-2	Sequence 2, Appli
43	363	17.8	411	11	US-09-892-360-18	Sequence 18, Appl
44	363	17.8	411	14	US-10-121-746-83	Sequence 83, Appl
45	363	17.8	411	16	US-10-745-210-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-939-484-4
; Sequence 4, Application US/09939484
; Patent No. US20020032322A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-00
; CURRENT APPLICATION NUMBER: US/09/939,484
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; TYPE: PRT
; LENGTH: 394
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-484-4

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Dd	1	MKRQNVETLALIVCTFTYLLVGA	VFDAL	ESEPELI	ERQRLELRQQL	RARYNL	SQG	GYE	60	
Qy	61	ELERVVLRLKPHKAGVQR	FAGS	FYPALT	VTTTIGYGHAAP	STDGGKVFCM	FYALLGIPL	120		
Dd	61	ELERVVLRLKPHKAGVQR	FAGS	FYPALT	VTTTIGYGHAAP	STDGGKVFCM	FYALLGIPL	120		
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Dd	121	TLVMFQSILGERINTLVRYLLHRAKKG	LGMRRADYSMAN	NWLI	GF	FS	CISTLCIGAAAF	SH	180	
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Dd	181	YEHWTFFQAYYYCIFTITLTGFGDYVAL	KDQALQTQPYVA	FSFVILTGLTVIGAFLN	240					
Qy	241	LVVLRFMTMAEDKRDAEHRALLTRNGACQ	GGGGGSAHTDTAS	TSTAAGGGGFRNVY	300					
Dd	241	LVVLRFMTMAEDKRDAEHRALLTRNGACQ	GGGGGSAHTDTAS	TSTAAGGGGFRNVY	300					
Qy	301	AEVLFHSQMSCCLWKYSREKLQYSIPMI	IIPDLSTSDTCVQSHSSPGCGGRYSDTPSR	360						
Dd	301	AEVLFHSQMSCCLWKYSREKLQYSIPMI	IIPDLSTSDTCVQSHSSPGCGGRYSDTPSR	360						
Qy	361	CLCSGARPRSAISSYSTGLHSLSTP	RGLMKRRSSV	394						
Dd	361	CLCSGARPRSAISSYSTGLHSLSTP	RGLMKRRSSV	394						

RESULT 2

US-09-939-483-4
; Sequence 4, Application US/09939483
; Patent No. US2002009458A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 4
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-483-4

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Db      121  TLVMFQSLGERINTLVRYLLHRAKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
Qy      181  YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTPQYVAESFVYILTGLTVIGAFLN 240
Db      181  YEHWTFFQAYYYCFITLTTIGFGDYVALQKDQALQTPQYVAESFVYILTGLTVIGAFLN 240
Qy      241  LVLRFTMWTMAEDBKDAEHRALLTRNGQAGGGGGGSAHTTDTASTAAAGGGGFNNVY 300
Db      241  LVLRFTMWTMAEDBKDAEHRALLTRNGQAGGGGGGSAHTTDTASTAAAGGGGFNNVY 300
Qy      301  AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSRR 360
Db      301  AEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSRR 360
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Db      361  CLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 3
US-09-798-584-15
; Sequence 15, Application US/09798584
; Patent No. US20020102676A1
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; TITLE OF INVENTION: KCN: A No. US20020102676A1el Potassium Channel Protein
; FILE REFERENCE: 018781-004010US
; CURRENT APPLICATION NUMBER: US/09/798,584
; CURRENT FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human potassium channel KCN3 (TASK1)
US-09-798-584-15

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	Query Match	100.0%	Score 2042;	DB 9;	Length 394;
	Best Local Similarity	100.0%;	Pred. No. 1.4e-180;		
	Matches 394;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MKRQNVETLALIVCTFTYLLVGAAVFDALSEPELIERQLELRQQLRARIYNLSQCGYE	60		
DB	1	MKRQNVETLALIVCTFTYLLVGAAVFDALSEPELIERQLELRQQLRARIYNLSQCGYE	60		
QY	61	ELERWVLRLLPKHGAGVQWRPAGSYFPAITVITTIYGCHAAPSTDGGKVFCMFFYALLGIPL	120		
DB	61	ELERWVLRLLPKHGAGVQWRPAGSYFPAITVITTIYGCHAAPSTDGGKVFCMFFYALLGIPL	120		
QY	121	TLNVFQSLGERINTLVRYLLHRAKKGLOMRADVSMANWVLIGFFSCISTLCIGAAAFSH	180		
DB	121	TLNVFQSLGERINTLVRYLLHRAKKGLOMRADVSMANWVLIGFFSCISTLCIGAAAFSH	180		
QY	181	YEHWTFFQAYYYCEITITLTIGFGDYVALQKDQALQTOQYVAFSFVYILTGLTVIGAPLN	240		
DB	181	YEHWTFFQAYYYCEITITLTIGFGDYVALQKDQALQTOQYVAFSFVYILTGLTVIGAPLN	240		
QY	241	LVVLRFTMTMADEKRDHAERHALLTRNGAGGGGGGSAHTTDTASSTAAGGGGFRNVY	300		
DB	241	LVVLRFTMTMADEKRDHAERHALLTRNGAGGGGGGSAHTTDTASSTAAGGGGFRNVY	300		
QY	301	AEVLHFOSMGCSLWYKGREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTSSRR	360		

Db 301 AEVLHFQSMCCLWYKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSDTPSRR 360
Qy 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394
Db 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394
RESULT 4
US-10-146-733-17
; Sequence 17, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
; TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-733-17
Query Match 100.0%; Score 2042; DB 14; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.4e-180;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MCRQNVRLALIVCTFTYLLVGAAYVDALESEPELLERORLELRQOELRARNYLSQGGYE 60
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Db 61 ELERVVLRLKPKHAGVQWRPAGSFYFAITVITTTIGYGHAAAPSTDGKGVCFMCFYALLGIPL 120
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Db 121 TLVMEFQSLGERINTLVRYLLHRAKGLGMRRAVDSNMNMVLIIGFFSCISTLCIGAAAFSH 180
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Db 181 YEHWTFFQAYYYCFITLTITIGFDYVALQKQDALQTOPOYVAFSFYIITGLTVIGAFLN 240
Qy 241 LVVLFPMTNWABDEKRDHRAKGLGMRRAVDSNMNMVLIIGFFSCISTLCIGAAAFSH 300
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Db 301 AEVLHFQSMCCLWYKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSDTPSRR 360
Qy 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394
Db 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394
RESULT 5
US-10-146-733-18
; Sequence 18, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
; TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/796,720
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/833,081
; PRIOR FILING DATE: 2001-04-11

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; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-733-18

Query Match      100.0%; Score 2042; DB 14; Length 394;
Best Local Similarity 100.0%; Pred. No. 1.4e-180;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKRQNVRLALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRQELRARNYLSQGGYE 60

Qy 61 ELERVVLRLKPKHKGAVQWRFGSFYFAITVTTTIGYGHAAFPSTDGKVFYALLGIPL 120
Db 61 ELERVVLRLKPKHKGAVQWRFGSFYFAITVTTTIGYGHAAFPSTDGKVFYALLGIPL 120

Qy 121 TLVMFQSLGERINTLVRYLLHRAKGLGWRADVSMANNVLIIGFPPSCISTLCIGAAAFSH 180
Db 121 TLVMFQSLGERINTLVRYLLHRAKGLGWRADVSMANNVLIIGFPPSCISTLCIGAAAFSH 180

Qy 181 YEHWTFQAYYFCITLTIGFDYVALQKQALQTPQYVAFSVYILTGLTVIGAFLN 240
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Db 301 AEVLHFQSMCCLWYKSKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSDTPSR 360

Qy 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394
Db 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394

RESULT 6
US-10-146-733-8
; Sequence 8, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
; TITLE OF INVENTION: NMMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
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; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/796,720
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/833,081
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-733-8

Query Match      100.0%; Score 2042; DB 14; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.4e-180;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 MKRQNVRLALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRQELRARNYLSQGGYE 61

Qy 61 ELERVVLRLKPKHKGAVQWRFGSFYFAITVTTTIGYGHAAFPSTDGKVFYALLGIPL 120
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Db 182 YEHWTFQAYYFCITLTIGFDYVALQKQALQTPQYVAFSVYILTGLTVIGAFLN 241

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Db 242 LVVLFMTNNAEDEKRAHRAHLLTRNGQAGGGGGGSAHTTDTASSTAAAGGGGRNYY 301

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Db 302 AEVLHFQSMCCLWYKSKREKLQYSIPMIIPDLSTSDTCVEQSHSPGGGGRYSDTPSR 361

Qy 361 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 394
Db 362 CLCSGAPRSATSSVSTGLHSLSTFRGLMKRRSSV 395
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RESULT 7
US-10-146-733-9
; Sequence 9, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtie, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silob-Santiago, Immaculada
; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
; TITLE OF INVENTION: HMMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: MNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/796,720
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/833,081
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-146-733-9

Query Match 90.6%; Score 1850.5; DB 14; Length 412;
Best Local Similarity 88.3%; Pred. No. 8.3e-163;
Matches 363; Conservative 8; Mismatches 23; Indels 17; Gaps 2;

QY 1 MKRONVRLALVCTFTYLLVGAAVFDALSEPELIERORLELRQELRARNYLSGGYE 60
DB 2 MKRONVRLALVCTFTYLLVGAAVFDALSEPELIERORLELRQELRARNYLSGGYE 61

QY 61 ELERVRLKPKHAGVQWRPAGSFYFAITVITIGYHAAAPSTDGKVFCEMFIPL 120
DB 62 ELERVRLKPKHAGVQWRPAGSFYFAITVITIGYHAAAPSTDGKVFCEMFIPL 121

QY 121 TLVFMFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFSCISTLCIGAAAFSH 180
DB 122 TLVFMFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFSCISTLCIGAAAFSV 181
QY 181 YEHWTFFQAYYYCFITLTITIGFDYVALQDQALQTOPOYVAFSVFYLLTGLTVIGAPLN 240
DB 182 YERWTFFQAYYYCFITLTITIGFDYVALQDQALQTOPOYVAFSVFYLLTGLTVIGAPLN 241
QY 241 LVVLFMTNNADEKRDADHRAHLLTRNGQAGGGG-----GGSAAHTTTDTASSTAAA- 291
DB 242 LVVLFMTNNADEKRDADHRAHLLTRNGQAGGGGSLGSLGSLGSLGSLGSLGSLGSLGSLG 301
QY 292 -----GGGGRNRYAELVLFQSWCSCLYKSKREKLYSIPMIIPDLSTSDTVCVEOS 343
DB 302 GMGVGVGVGGSGFRNRYAELVLFQSWCSCLYKSKREKLYSIPMIIPDLSTSDTVCVEOS 361
QY 344 HSSPGGGGRYSDTPSRRLCLSCGAPSAISSVSTGLHSLSTFRGLMKRRSSV 394
DB 362 HSSPGGGGRYSDTPSRRLCLSCGAPSAISSVSTGLHSLSTFRGLMKRRSSV 412

RESULT 8
US-09-939-484-5
; Sequence 5, Application US/09939484
; Patent No. US2002003232A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-00
; CURRENT APPLICATION NUMBER: US/09/939,484
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-484-5

Query Match 89.1%; Score 1819; DB 9; Length 405;
Best Local Similarity 88.1%; Pred. No. 6.8e-160;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;

QY 4 QNVRTLALVCTFTYLLVGAAVFDALSEPELIERORLELRQELRARNYLSGGYE 63
DB 1 NVRTLALVCTFTYLLVGAAVFDALSEPELIERORLELRQELRARNYLSGGYE 60

QY 64 RVVRLKPKHAGVQWRPAGSFYFAITVITIGYHAAAPSTDGKVFCEMFIPL 123
DB 61 RVVRLKPKHAGVQWRPAGSFYFAITVITIGYHAAAPSTDGKVFCEMFIPL 120

QY 124 MFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFSCISTLCIGAAAFSHYEH 183
DB 121 MFQSLGERINTLVRYLLHRAKGLGMRADVSMANMVLIGFFSCISTLCIGAAAFSVYER 180

QY 184 WTFQAYYYCFITLTITIGFDYVALQDQALQTOPOYVAFSVFYLLTGLTVIGAPLN 243
DB 181 WTFQAYYYCFITLTITIGFDYVALQDQALQTOPOYVAFSVFYLLTGLTVIGAPLN 240

QY 244 LRFMTMNAEDEKRDHALLTRNGOAGGGG-----GSAHTTDTASSTAAA----- 291
Db 241 LRFMTMNAEDEKRDHALLTHNGOAVGLGSLCCLSGSLGSDVRPRDPVTCAAAAGGVGV 300
QY 292 --GGGGRNVYAEVLHFQSMCSCLWYKREKLOYSIPMIIPRDLSTSDTCVEQSHSSPGG 349
Db 301 GVGSGFRNVYAEVLHFQSMCSCLWYKREKLOYSIPMIIPRDLSTSDTCVEHSHSSPGG 360
QY 350 GGRYSDTPSRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
Db 361 GGRYSDTPSHPCCLSGTQRSATSISSVSTGLHSLAARGLMKRRSSV 405
RESULT 9
US-09-939-483-5
; Sequence 5, Application US/09939483
; Patent No. US20020094558A1
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 1201-CIP-DIV-2-00
; CURRENT APPLICATION NUMBER: US/09/939,483
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/144,914
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 08/749,816
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/095,234
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: FR 96/01565
; PRIOR FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-939-483-5
Query Match 89.1%; Score 1819; DB 9; Length 405;
Best Local Similarity 88.1%; Pred. No. 6.8e-160;
Matches 357; Conservative 9; Mismatches 25; Indels 14; Gaps 2;
QY 4 QNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLERQLELRARYNLSQGGYELE 63
Db 1 ENVRTALIVCTFTYLLVGAADFDALESEPEMIERQRLERQLELRARYNLSQGGYELE 60
QY 64 RVVLRKPKHAGVQWRPAGSFYFAITVTITIGYHAAAPSTDGKVFYFALLGPIPLV 123
Db 61 RVVLRKPKHAGVQWRPAGSFYFAITVTITIGYHAAAPSTDGKVFYFALLGPIPLI 120
QY 124 MFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVLIGFVSCISTLCIGAAAFSHYEH 183
Db 121 MFQSLGERINTFVRYLLHRAKGLGMRHAEVSMANNVLIGFVSCISTLCIGAAAFSYER 180
QY 184 WTFPQAYYYCFITLTITIGFDYVALQKQALQTOQYVAFSPVYILTGLTVIGAFNLV 243
Db 181 WTFPQAYYYCFITLTITIGFDYVALQKQALQTOQYVAFSPVYILTGLTVIGAFNLV 240
QY 244 LRFMTMNAEDEKRDHALLTRNGOAGGGG-----GSAHTTDTASSTAAA----- 291
Db 241 LRFMTMNAEDEKRDHALLTHNGOAVGLGSLCCLSGSLGSDVRPRDPVTCAAAAGGVGV 300
QY 292 --GGGGRNVYAEVLHFQSMCSCLWYKREKLOYSIPMIIPRDLSTSDTCVEQSHSSPGG 349
Db 301 GVGSGFRNVYAEVLHFQSMCSCLWYKREKLOYSIPMIIPRDLSTSDTCVEHSHSSPGG 360

QY 350 GGRYSDTPSRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
Db 361 GGRYSDTPSHPCCLSGTQRSATSISSVSTGLHSLAARGLMKRRSSV 405
RESULT 10
US-09-746-491-61
; Sequence 61, Application US/09746491
; Patent No. US20020137202A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20020137202A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-621
; CURRENT APPLICATION NUMBER: US/09/746,491
; CURRENT FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: USN 60/171,329
; PRIOR FILING DATE: 1999-12-21
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 61
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-746-491-61
Query Match 62.6%; Score 1278; DB 9; Length 258;
Best Local Similarity 96.1%; Pred. No. 5.7e-110;
Matches 248; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 1 MKQNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLERQLELRARYNLSQGGYE 60
Db 1 MKQNVRTLALIVCTFTYLLVGAADFDALESEPEMIERQRLERQLELRARYNLSQGGYE 60
QY 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVTITIGYHAAAPSTDGKVFYFALLGPIPL 120
Db 61 ELERVVLRKPKHAGVQWRPAGSFYFAITVTITIGYHAAAPSTDGKVFYFALLGPIPL 120
QY 121 TLVNFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVLIGFVSCISTLCIGAAAFSH 180
Db 121 TLVNFQSLGERINTFVRYLLHRAKGLGMRHAEVSMANNVLIGFVSCISTLCIGAAAFSY 180
QY 181 YEHWTFFQAYYYCFITLTITIGFDYVALQKQALQTOQYVAFSPVYILTGLTVIGAFNL 240
Db 181 YERWTFQAYYYCFITLTITIGFDYVALQKQALQTOQYVAFSPVYILTGLTVIGAFNL 240
QY 241 LVVLRFTMTMNAEDEKRD 258
Db 241 LVVLRFTMTMNAEDEKRD 258
RESULT 11
US-08-816-011-55
; Sequence 55, Application US/08816011
; Publication No. US20030165806A1
; GENERAL INFORMATION:
; APPLICANT: Price, Laura A.
; APPLICANT: Fausch, Mark H.
; TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
; TITLE OF INVENTION: Encoding Them, and Methods of Using Same
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Home Products Corporation
; STREET: One Campus Drive
; CITY: Parsippany
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,011
; FILING DATE: 11-MAR-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthews, Gale F.
; REGISTRATION NUMBER: 32,269
; REFERENCE/DOCKET NUMBER: 32,421-C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-683-2134
; TELEFAX: 201-683-4117
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 312 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-816-011-55

Query Match          59.9%; Score 1224; DB 8; Length 312;
Best Local Similarity 83.1%; Pred. No. 7.4e-105;
Matches 250; Conservative 8; Mismatches 27; Indels 16; Gaps 4;

QY      4 QNVRTLALIVCTFTYLLVGAAVFDALESEPELIERORLELRQOELRARNYLSGGYEEL 63
Db      13 ENVRTLALIVCTFTYLLVGAAVFDALESEPEMERORLELRQELRARNYLSGGYEEL 72

QY      64 RVVLRKPKHKGQVWRFAGSFYFAITVITTYGHAAPSTDGKGV---FCMFYALLGIPL 120
Db      73 RVVLRKPKHKGQVWRFAGSFYFAITVITTYGHAAPSTDGKGVCMFCMFYALLGIPL 132

QY      121 TLVMSFQSLGERINTLVRYLLHRAKGLGMRRAADVSMANMVLIGFFSCISTLCIGAAAFSH 180
Db      133 TLVMSFQSLGERINTSVRYLLHRAKGLGMRHAEVSMANMVLIGFVSCISTLCIGAAAFSY 192

QY      181 YEHWTFFQAYYYCFITLTITIGDYVALQKQALQTPQYVAFSFYVILTGLTVIG--AF 238
Db      193 YERWTFQAYYYCFITLTITIGDYVALQKQALQTPQYVAFSVA---SCTSSRAHGHRF 249

QY      239 LNLVLRFTWMADEKRAEHRALLTRNGQAGGGG-----GSAHTTDTASSTAA 290
Db      250 LNLVLRFTWMADEKRAEHRALLTHNGQAVLGSLGSLSGLDGVRPRDPTVCAAA 309

QY      291 A 291
Db      310 A 310

RESULT 12
US-10-870-492-55
; Sequence 55, Application US/10870492
; Publication No. US20050032165A1
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; AND METHODS OF USING SAME
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/816,011
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Mus musculus

Query Match          59.9%; Score 1224; DB 8; Length 312;
Best Local Similarity 83.1%; Pred. No. 7.4e-105;
Matches 250; Conservative 8; Mismatches 27; Indels 16; Gaps 4;

QY      4 QNVRTLALIVCTFTYLLVGAAVFDALESEPELIERORLELRQOELRARNYLSGGYEEL 63
Db      13 ENVRTLALIVCTFTYLLVGAAVFDALESEPEMERORLELRQELRARNYLSGGYEEL 72

QY      64 RVVLRKPKHKGQVWRFAGSFYFAITVITTYGHAAPSTDGKGV---FCMFYALLGIPL 120
Db      73 RVVLRKPKHKGQVWRFAGSFYFAITVITTYGHAAPSTDGKGVCMFCMFYALLGIPL 132

QY      121 TLVMSFQSLGERINTLVRYLLHRAKGLGMRRAADVSMANMVLIGFFSCISTLCIGAAAFSH 180
Db      133 TLVMSFQSLGERINTSVRYLLHRAKGLGMRHAEVSMANMVLIGFVSCISTLCIGAAAFSY 192

QY      181 YEHWTFFQAYYYCFITLTITIGDYVALQKQALQTPQYVAFSFYVILTGLTVIG--AF 238
Db      193 YERWTFQAYYYCFITLTITIGDYVALQKQALQTPQYVAFSVA---SCTSSRAHGHRF 249

QY      239 LNLVLRFTWMADEKRAEHRALLTRNGQAGGGG-----GSAHTTDTASSTAA 290
Db      250 LNLVLRFTWMADEKRAEHRALLTHNGQAVLGSLGSLSGLDGVRPRDPTVCAAA 309

QY      291 A 291
Db      310 A 310

RESULT 13
US-10-459-190-15
; Sequence 15, Application US/10459190
; Publication No. US20040072216A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Palma, John F.
; APPLICANT: Schweitzer, Anthony C.
; APPLICANT: Blume, John E.
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; TITLE OF INVENTION: Diabetes
; FILE REFERENCE: 016325-0082100S
; CURRENT APPLICATION NUMBER: US/10/459,190
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/387,642
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: transmembrane (TM) and pore domains of mouse
; OTHER INFORMATION: TWIK-related acid-sensitive potassium channel 1
; OTHER INFORMATION: (TASK-1)
;
US-10-459-190-15

Query Match          56.5%; Score 1154; DB 15; Length 233;
Best Local Similarity 95.7%; Pred. No. 1.6e-98;
Matches 223; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      7 RTLALIVCTFTYLLVGAAVFDALESEPELIERORLELRQOELRARNYLSGGYEELRVV 66
Db      1 RTLALIVCTFTYLLVGAAVFDALESEPEMERORLELRQELRARNYLSGGYEELRVV 60

QY      67 LRLKPKHKGQVWRFAGSFYFAITVITTYGHAAPSTDGKGVCMFCMFYALLGIPLTVMFQ 126
Db      61 LRLKPKHKGQVWRFAGSFYFAITVITTYGHAAPSTDGKGVCMFCMFYALLGIPLTVMFQ 120

QY      127 SLGERINTLVRYLLHRAKGLGMRRAADVSMANMVLIGFFSCISTLCIGAAAFSHYHWT 186
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US-10-870-492-55

Query Match          59.9%; Score 1224; DB 17; Length 312;
Best Local Similarity 83.1%; Pred. No. 7.4e-105;
Matches 250; Conservative 8; Mismatches 27; Indels 16; Gaps 4;

QY      4 QNVRTLALIVCTFTYLLVGAAVFDALESEPELIERORLELRQOELRARNYLSGGYEEL 63
Db      13 ENVRTLALIVCTFTYLLVGAAVFDALESEPEMERORLELRQELRARNYLSGGYEEL 72

QY      64 RVVLRKPKHKGQVWRFAGSFYFAITVITTYGHAAPSTDGKGV---FCMFYALLGIPL 120
Db      73 RVVLRKPKHKGQVWRFAGSFYFAITVITTYGHAAPSTDGKGVCMFCMFYALLGIPL 132

QY      121 TLVMSFQSLGERINTLVRYLLHRAKGLGMRRAADVSMANMVLIGFFSCISTLCIGAAAFSH 180
Db      133 TLVMSFQSLGERINTSVRYLLHRAKGLGMRHAEVSMANMVLIGFVSCISTLCIGAAAFSY 192

QY      181 YEHWTFFQAYYYCFITLTITIGDYVALQKQALQTPQYVAFSFYVILTGLTVIG--AF 238
Db      193 YERWTFQAYYYCFITLTITIGDYVALQKQALQTPQYVAFSVA---SCTSSRAHGHRF 249

QY      239 LNLVLRFTWMADEKRAEHRALLTRNGQAGGGG-----GSAHTTDTASSTAA 290
Db      250 LNLVLRFTWMADEKRAEHRALLTHNGQAVLGSLGSLSGLDGVRPRDPTVCAAA 309

QY      291 A 291
Db      310 A 310

RESULT 13
US-10-459-190-15
; Sequence 15, Application US/10459190
; Publication No. US20040072216A1
; GENERAL INFORMATION:
; APPLICANT: Johnson, Jeffrey D.
; APPLICANT: Palma, John F.
; APPLICANT: Schweitzer, Anthony C.
; APPLICANT: Blume, John E.
; APPLICANT: Metabolex, Inc.
; TITLE OF INVENTION: Methods and Compositions for Treating and Diagnosing
; TITLE OF INVENTION: Diabetes
; FILE REFERENCE: 016325-0082100S
; CURRENT APPLICATION NUMBER: US/10/459,190
; CURRENT FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: US 60/387,642
; PRIOR FILING DATE: 2002-06-10
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Mus sp.
; FEATURE:
; OTHER INFORMATION: transmembrane (TM) and pore domains of mouse
; OTHER INFORMATION: TWIK-related acid-sensitive potassium channel 1
; OTHER INFORMATION: (TASK-1)
;
US-10-459-190-15

Query Match          56.5%; Score 1154; DB 15; Length 233;
Best Local Similarity 95.7%; Pred. No. 1.6e-98;
Matches 223; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY      7 RTLALIVCTFTYLLVGAAVFDALESEPELIERORLELRQOELRARNYLSGGYEELRVV 66
Db      1 RTLALIVCTFTYLLVGAAVFDALESEPEMERORLELRQELRARNYLSGGYEELRVV 60

QY      67 LRLKPKHKGQVWRFAGSFYFAITVITTYGHAAPSTDGKGVCMFCMFYALLGIPLTVMFQ 126
Db      61 LRLKPKHKGQVWRFAGSFYFAITVITTYGHAAPSTDGKGVCMFCMFYALLGIPLTVMFQ 120

QY      127 SLGERINTLVRYLLHRAKGLGMRRAADVSMANMVLIGFFSCISTLCIGAAAFSHYHWT 186
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Db 121 SLGERINTFVRLHRAKGLGMRHAEVSMANVLLIGFVSCISTLCIGAAAFSYVERWTF 180
QY 187 FOAYYYCFTITTTIGFDYVALQKQALQTOQYVAFSFVYILTGLTVIGAF 239
Db 181 FOAYYYCFTITTTIGFDYVALQKQALQTOQYVAFSFVYILTGLTVIGAF 233

RESULT 14

US-09-798-584-1
; Sequence 1, Application US/09798584
; Patent No. US20020102676A1
; GENERAL INFORMATION:
; APPLICANT: Mu, David
; APPLICANT: Powers, Scott
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: KCNB: A No. US20020102676A1el Potassium Channel Protein
; FILE REFERENCE: 018781-004010US
; CURRENT APPLICATION NUMBER: US/09/798,584
; PRIOR FILING DATE: 2001-03-03
; PRIOR APPLICATION NUMBER: US 60/186,951
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human KCNB (Potassium Channel expressed in Breast)
US-09-798-584-1

Query Match 54.7%; Score 1116; DB 9; Length 374;
Best Local Similarity 59.0%; Pred. No. 9.7e-95;
Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

QY 1 MKRQNVRTIALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARNYLSQGGYE 60
Db 1 MKRQNVRTLSLVCTFTYLLVGAADFDALESDHEMREBEKKAERIRKGNYSSEYR 60
QY 61 ELERVLLRKPKHAGVQWRPAGSFYFAITVTTIGYHAAAPSTDGKVFQVCFMYALLGIPL 120
Db 61 QLEVLQSEPHRAGVQWKFGSFYFAITVTTIGYHAAAPSTDGKAFQVCFMYALLGIPL 120
QY 121 TLVMFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVLLIGFSCISTLCIGAAAFSH 180
Db 121 TLVMFQSLGERMNTFVRYLLKRIKCCGMRNTDVMENNVTGVFFSCMTLCIGAAAFSQ 180
QY 181 YEHWTFFQAYYYCFTITTTIGFDYVALQKQALQTOQYVAFSFVYILTGLTVIGAF 240
Db 181 CEWSFFHAYYYCFTITTTIGFDYVALQKQALQKPLLYVAFSPWYILVGLTVIGAF 240
QY 241 LVVLRFTMTNABDEKRADEHRAALLTRNGOAGGGGGGSAHTTDTASSTAAGGGGRNYY 300
Db 241 LVVLRFTMTNABDEKRADEHRAALLTRNGOAGGGGGGSAHTTDTASSTAAGGGGRNYY 300
QY 301 -REVLFHFSQCMCLMYKREKQYISPMIIPDLSTSDTCVQSHSSPGGGRYSDTSR 359
Db 287 KADVPDLPQVCSCTCYRQD---YGRSVAPQNSFSAKLAPHYFHSISYKIEISPTLK 343
QY 360 RCLCSGAPRASAISVSTGLHLSLSTRGLMKRSSV 394
Db 344 NSLFP----SPISSISPLHLSHSTDRQLMKRKS 374

RESULT 15

US-10-146-733-41
; Sequence 41, Application US/10146733
; Publication No. US20030165891A1
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Silos-Santiago, Inmaculada

; TITLE OF INVENTION: NOVEL TWIK-6, TWIK-7, IC23927, TWIK-8, IC47611, IC47615,
; TITLE OF INVENTION: HNMDA-1, TWIK-9, alpha2delta-4, 54414, AND 53763 MOLECULES
; FILE REFERENCE: MNI-248
; CURRENT APPLICATION NUMBER: US/10/146,733
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US 60/185,938
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/515,520
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/518,866
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: US 60/195,734
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: US 60/195,993
; PRIOR FILING DATE: 2000-04-11
; PRIOR APPLICATION NUMBER: US 60/199,799
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: US 60/233,537
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: US 60/235,018
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/235,059
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US 60/256,240
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/256,588
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/258,028
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/796,720
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/828,035
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 09/833,081
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: US 09/843,128
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: US 09/957,683
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: US 09/964,252
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 09/964,256
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 10/024,623
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 41
; LENGTH: 374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-146-733-41
Query Match 54.7%; Score 1116; DB 14; Length 374;
Best Local Similarity 59.0%; Pred. No. 9.7e-95;
Matches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;
QY 1 MKRQNVRTIALIVCTFTYLLVGAADFDALESEPELIERQRLRQELRARNYLSQGGYE 60
Db 1 MKRQNVRTLSLVCTFTYLLVGAADFDALESDHEMREBEKKAERIRKGNYSSEYR 60
QY 61 ELERVLLRKPKHAGVQWRPAGSFYFAITVTTIGYHAAAPSTDGKVFQVCFMYALLGIPL 120
Db 61 QLEVLQSEPHRAGVQWKFGSFYFAITVTTIGYHAAAPSTDGKAFQVCFMYALLGIPL 120
QY 121 TLVMFQSLGERINTLVRYLLHRAKGLGMRADVSMANNVLLIGFSCISTLCIGAAAFSH 180
Db 121 TLVMFQSLGERMNTFVRYLLKRIKCCGMRNTDVMENNVTGVFFSCMTLCIGAAAFSQ 180
QY 181 YEHWTFFQAYYYCFTITTTIGFDYVALQKQALQTOQYVAFSFVYILTGLTVIGAF 240
Db 181 CEWSFFHAYYYCFTITTTIGFDYVALQKQKPLLYVAFSPWYILVGLTVIGAF 240

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QY 241 LVVLRPMTWNAEDEKRDADAEHRALLTRNGQAGCGGGGSAHTTDTASSTAAGGGFRNVY 300
Db 241 LVVLRFLTMNSEDERDAEERASL-----AGNRNSMVIHIPEERPS-----RPRY 286
QY 301 -AEVLHFQSMCCLWYKREKLOYISIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSR 359
Db 287 KADVPLQSVCSCTCYRSQP---YGGRSVAPQNSFSAKLAPHYFHSISYKIEISFSTLK 343
QY 360 RCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV 394
Db 344 NSLFP----SPISSISPLHSTFDHQLMKRRKSV 374
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Search completed: July 13, 2005, 09:07:02
Job time : 87.5115 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:10:49 ; Search time 25.273 Seconds
(without alignments)
1163.760 Million cell updates/sec

Title: US-09-503-089A-5
Perfect score: 2042
Sequence: 1 MKRQNVRLALIVCTFTYLL.....STGLHSLSTFRGLMKRRSV 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/prodata/1/1aa/5B-COMB.pep:*
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5: /cgn2_6/prodata/1/1aa/PCTUS-COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2042	100.0	394	US-09-144-914-4	Sequence 4, Appli
2	1819	89.1	405	US-09-144-914-5	Sequence 5, Appli
3	1116	54.7	388	US-09-949-016-7631	Sequence 7631, Ap
4	773	37.9	408	US-09-362-842-12	Sequence 12, Appl
5	379	18.6	361	US-09-362-842-14	Sequence 14, Appl
6	370	18.1	370	US-09-144-914-8	Sequence 8, Appli
7	369	18.1	411	US-09-236-080-6	Sequence 6, Appli
8	363	17.8	411	US-09-236-080-2	Sequence 2, Appli
9	363	17.8	411	US-09-336-643A-83	Sequence 83, Appl
10	349.5	17.1	538	US-09-949-016-7001	Sequence 7001, Ap
11	349.5	17.1	558	US-09-949-016-7368	Sequence 7368, Ap
12	329.5	16.1	393	US-09-432-470-2	Sequence 2, Appli
13	329.5	16.1	393	US-09-432-470-4	Sequence 4, Appli
14	329.5	16.1	419	US-09-949-016-6913	Sequence 6913, Ap
15	329.5	16.1	440	US-09-949-016-7809	Sequence 7809, Ap
16	320.5	15.7	336	US-08-749-816-2	Sequence 2, Appli
17	320.5	15.7	336	US-09-144-914-2	Sequence 2, Appli
18	319	15.6	499	US-09-561-763-2	Sequence 2, Appli
19	319	15.6	499	US-09-431-367B-2	Sequence 2, Appli
20	312	15.3	146	US-09-362-842-69	Sequence 69, Appl
21	312	15.3	146	US-09-270-767-31685	Sequence 31685, A
22	295.5	14.5	313	US-09-336-643A-81	Sequence 81, Appl
23	295.5	14.5	313	US-09-561-763-8	Sequence 8, Appli
24	295.5	14.5	313	US-09-431-367B-8	Sequence 8, Appli
25	294.5	14.4	332	US-09-561-763-5	Sequence 5, Appli
26	294.5	14.4	332	US-09-431-367B-5	Sequence 5, Appli
27	278.5	13.6	995	US-09-362-842-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-144-914-4
; Sequence 4, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989 6705CJP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: TASK
US-09-144-914-4

Query Match 100.0%; Score 2042; DB 3; Length 394;
Best Local Similarity 100.0%; Pred. No. 7.8e-217;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKRQNVRLALIVCTFTYLLVGAAVFDALASEPELIERQRLERQELRARNLSQGGYE 60
DB 1 MKRQNVRLALIVCTFTYLLVGAAVFDALASEPELIERQRLERQELRARNLSQGGYE 60
QY 61 ELERVVLRLKPKHAGVQWRFGAGSYFAITVITTYGHAAPSTDGKVFQCMFYALIGIPL 120
DB 61 ELERVVLRLKPKHAGVQWRFGAGSYFAITVITTYGHAAPSTDGKVFQCMFYALIGIPL 120
QY 121 TLVMPQSLGERINTLVRYLLHRKGLGNRRADVSMMNVLIQGFSCISTLCIGAAAFSH 180
DB 121 TLVMPQSLGERINTLVRYLLHRKGLGNRRADVSMMNVLIQGFSCISTLCIGAAAFSH 180
QY 181 YEHWTFFQAYYYCFTLTITIGFDVVALQDQALQTOQYVAFSVYILTGLTVTGAFUN 240
DB 181 YEHWTFFQAYYYCFTLTITIGFDVVALQDQALQTOQYVAFSVYILTGLTVTGAFUN 240

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Qy 241 LVVLRFTMNAEDEKRAEHRALLTRNGAAGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300
Db 241 LVVLRFTMNAEDEKRAEHRALLTRNGAAGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300
Qy 301 AEVLHFQSMCWLKYSREKLQYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSRR 360
Db 301 AEVLHFQSMCWLKYSREKLQYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSRR 360
Qy 361 CLCSGAPRSATSSVSTGLHSLSTRGLMKRRSSV 394
Db 361 CLCSGAPRSATSSVSTGLHSLSTRGLMKRRSSV 394

RESULT 2
US-09-144-914-5
; Sequence 5, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Fink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989,6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TASK
US-09-144-914-5

Query Match 89.1%; Score 1819; DB 3; Length 405;
Best Local Similarity 88.1%; Pred. No. 3.6e-192; Mismatches 25; Indels 14; Gaps 2;
Matches 357; Conservative 9;

Qy 4 QNVRTALIVCTFTYLLVGAADFDALESEPELIERQRLERQELRRLRARNLSOGGYEEL 63
Db 1 ENVRTALIVCTFTYLLVGAADFDALESEPELIERQRLERQELRRLRARNLSOGGYEEL 60
Qy 64 RVVLRKPKHAGVQWRFGSFYFAITVTITIGYHAAAPSTDGKVFYFALLGIPLTLV 123
Db 61 RVVLRKPKHAGVQWRFGSFYFAITVTITIGYHAAAPSTDGKVFYFALLGIPLTLI 120
Qy 124 MFQSLGERINTLVRYLLHRAKGLGMRRADYSMMANNVLIGFSCISTICIGAAAFSHYEH 183
Db 121 MFQSLGERINTLVRYLLHRAKGLGMRRADYSMMANNVLIGFSCISTICIGAAAFSYER 180
Qy 184 WTFQFAYYCFITLTITIGFDYVALQDQALQTPQYVAFSPVYILTGLTVIGAFNLV 243
Db 181 WTFQFAYYCFITLTITIGFDYVALQDQALQTPQYVAFSPVYILTGLTVIGAFNLV 240
Qy 244 LRFMTMNAEDEKRAEHRALLTRNGAAGGGG-----GGSAHTTDTASSTAA----- 291
Db 241 LRFMTMNAEDEKRAEHRALLTRNGAAGGGG-----GGSAHTTDTASSTAA----- 291
Qy 292 --GGGGRFNVVAEVLHFQSMCWLKYSREKLQYSIPMIIPRDLSTSDTCVEQSHSPGG 349
Db 301 GVGSGFRNVVAEVLHFQSMCWLKYSREKLQYSIPMIIPRDLSTSDTCVEHSHSPGG 360
Qy 350 GGRYSDTPSRRCLCSGAPRSATSSVSTGLHSLSTRGLMKRRSSV 394
Db 350 GGRYSDTPSRRCLCSGAPRSATSSVSTGLHSLSTRGLMKRRSSV 394
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Db 361 GGRYSDTPSRRCLCSGAPRSATSSVSTGLHSLSTRGLMKRRSSV 405

RESULT 3
US-09-949-016-7631
; Sequence 7631, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7631
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7631

Query Match 54.7%; Score 1116; DB 4; Length 388;
Best Local Similarity 59.0%; Pred. No. 1.7e-114; Mismatches 233; Conservative 44; Mismatches 96; Indels 22; Gaps 5;

Qy 1 MKRQNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLERQELRRLRARNLSOGGYE 60
Db 15 MKRQNVRTLALIVCTFTYLLVGAADFDALESEPELIERQRLERQELRRLRARNLSOGGYE 74
Qy 61 ELERVVLRKPKHAGVQWRFGSFYFAITVTITIGYHAAAPSTDGKVFYFALLGIPL 120
Db 75 QLELVILQSEPHRAGVQWKFGSFYFAITVTITIGYHAAAPSTDGKVFYFALLGIPL 134
Qy 121 TLVVFQSLGERINTLVRYLLHRAKGLGMRRADYSMMANNVLIGFSCISTICIGAAAFSH 180
Db 135 TLVVFQSLGERINTLVRYLLHRAKGLGMRRADYSMMANNVLIGFSCISTICIGAAAFSQ 194
Qy 181 YEHTFQAYYCFITLTITIGFDYVALQDQALQTPQYVAFSPVYILTGLTVIGAFNL 240
Db 195 CEWSFHHAYYCFITLTITIGFDYVALQDQALQTPQYVAFSPVYILTGLTVIGAFNL 254
Qy 241 LVVLRFTMNAEDEKRAEHRALLTRNGAAGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300
Db 255 LVVLRFTMNAEDEKRAEHRALLTRNGAAGGGGGGSAHTTDTASSTAAAGGGGFRNVY 300
Qy 301 -AEVLHFQSMCWLKYSREKLQYSIPMIIPRDLSTSDTCVEQSHSPGGGGRYSDTPSR 359
Db 301 KADVPDLQSVCSCTCRSQD---YGGRSVAPQNSFSAKLAPHYFHSYKIEISPSPTLK 357
Qy 360 RCLCSGAPRSATSSVSTGLHSLSTRGLMKRRSSV 394
Db 358 NSLFP-----SPSSISPLHSHFTDHRMLMKRRKSV 388

RESULT 4
US-09-362-842-12
; Sequence 12, Application US/09362842
; Patent No. 6511824
; GENERAL INFORMATION:
; APPLICANT: Buchman et al.
; TITLE OF INVENTION: NUCLEIC ACIDS AND POLYPEPTIDES OF INVERTEBRATE TWIK
; TITLE OF INVENTION: CHANNELS AND METHODS OF USE
; FILE REFERENCE: 7326-104
; CURRENT APPLICATION NUMBER: US/09/362,842
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 09/270,767
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RESULT 7
US-09-236-080-6
; Sequence 6, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PR1
; ORGANISM: Mus musculus
US-09-236-080-6

Query Match      18.1%; Score 369; DB 3; Length 411;
Best Local Similarity 31.6%; Pred. No. 7.le-32;
Matches 93; Conservative 57; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRQVRLALIVCTFTYLLVGAAYFVDALESEPELIERQRLERQELRARNLSQGGYE 60
DB 42 MKWKTGSTIFLVV--VLYLIIGAAVFKALEQOEISQRTTIVIQKTFIAQHACVNS--T 97
QY 61 ELERVVRL-KPHKAGV-----QWRPAGSFYFAITVITTYGHAAPSTDDGKV 108
DB 98 ELDELIQIIVAAINAGIIPLGNSNQSHWDLGSSFFAGTVITTTIGFNGISPRTEGGKI 157
QY 109 FCMFYALLIGIPLTLMVQFSLGERINTLVRYLLHRAKKGGMERRAD-----VSM 156
DB 158 FCIYVALLIGIPFGFLAGVGDQGTIF-----GKGIKVEDTTFIKMNVSTQTKIRI 208
QY 157 ANMVLIGFSCISTLCIGAAAFSHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQT 216
DB 209 ISTIIFILGCVLFVALPAVFKHIEGWSALDAIVFVVTITLTIGFDYVAGGSD--IEY 266
QY 217 QPQYVAFSVYILGTGTIGVAFNLV--VLRFTWNAEDEKRD-AEHRALLTRN 267
DB 267 LDFYKPVVMFWILVGLAYFAAVLSMIGDWLRVISKTKKEEVGEFRAHAAEWATAN 320

Query Match      17.8%; Score 363; DB 3; Length 411;
Best Local Similarity 31.0%; Pred. No. 3.3e-31;
Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRQVRLALIVCTFTYLLVGAAYFVDALESEPELIERQRLERQELRARNLSQGGYE 60
DB 42 MKWKTGSTIFLVV--VLYLIIGAAVFKALEQOEISQRTTIVIQKTFISQHSVCNS--T 97
QY 61 ELERVVRL-KPHKAGV-----QWRPAGSFYFAITVITTYGHAAPSTDDGKV 108
DB 98 ELDELIQIIVAAINAGIIPLGNSNQSHWDLGSSFFAGTVITTTIGFNGISPRTEGGKI 157
QY 109 FCMFYALLIGIPLTLMVQFSLGERINTLVRYLLHRAKKGGMERRAD-----VSM 156
DB 158 FCIYVALLIGIPFGFLAGVGDQGTIF-----GKGIKVEDTTFIKMNVSTQTKIRI 208
QY 157 ANMVLIGFSCISTLCIGAAAFSHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQT 216
DB 209 ISTIIFILGCVLFVALPAVFKHIEGWSALDAIVFVVTITLTIGFDYVAGGSD--IEY 266
QY 217 QPQYVAFSVYILGTGTIGVAFNLV--VLRFTWNAEDEKRD-AEHRALLTRN 267
DB 267 LDFYKPVVMFWILVGLAYFAAVLSMIGDWLRVISKTKKEEVGEFRAHAAEWATAN 320

Query Match      17.8%; Score 363; DB 3; Length 411;
Best Local Similarity 31.0%; Pred. No. 3.3e-31;
Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRQVRLALIVCTFTYLLVGAAYFVDALESEPELIERQRLERQELRARNLSQGGYE 60
DB 42 MKWKTGSTIFLVV--VLYLIIGAAVFKALEQOEISQRTTIVIQKTFISQHSVCNS--T 97
QY 61 ELERVVRL-KPHKAGV-----QWRPAGSFYFAITVITTYGHAAPSTDDGKV 108
DB 98 ELDELIQIIVAAINAGIIPLGNSNQSHWDLGSSFFAGTVITTTIGFNGISPRTEGGKI 157
QY 109 FCMFYALLIGIPLTLMVQFSLGERINTLVRYLLHRAKKGGMERRAD-----VSM 156
DB 158 FCIYVALLIGIPFGFLAGVGDQGTIF-----GKGIKVEDTTFIKMNVSTQTKIRI 208
QY 157 ANMVLIGFSCISTLCIGAAAFSHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQT 216
DB 209 ISTIIFILGCVLFVALPAVFKHIEGWSALDAIVFVVTITLTIGFDYVAGGSD--IEY 266
QY 217 QPQYVAFSVYILGTGTIGVAFNLV--VLRFTWNAEDEKRD-AEHRALLTRN 267
DB 267 LDFYKPVVMFWILVGLAYFAAVLSMIGDWLRVISKTKKEEVGEFRAHAAEWATAN 320
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RESULT 8
US-09-236-080-2
; Sequence 2, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-236-080-2

Query Match      17.8%; Score 363; DB 3; Length 411;
Best Local Similarity 31.0%; Pred. No. 3.3e-31;
Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRQVRLALIVCTFTYLLVGAAYFVDALESEPELIERQRLERQELRARNLSQGGYE 60
DB 42 MKWKTGSTIFLVV--VLYLIIGAAVFKALEQOEISQRTTIVIQKTFISQHSVCNS--T 97
QY 61 ELERVVRL-KPHKAGV-----QWRPAGSFYFAITVITTYGHAAPSTDDGKV 108
DB 98 ELDELIQIIVAAINAGIIPLGNSNQSHWDLGSSFFAGTVITTTIGFNGISPRTEGGKI 157
QY 109 FCMFYALLIGIPLTLMVQFSLGERINTLVRYLLHRAKKGGMERRAD-----VSM 156
DB 158 FCIYVALLIGIPFGFLAGVGDQGTIF-----GKGIKVEDTTFIKMNVSTQTKIRI 208
QY 157 ANMVLIGFSCISTLCIGAAAFSHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQT 216
DB 209 ISTIIFILGCVLFVALPAVFKHIEGWSALDAIVFVVTITLTIGFDYVAGGSD--IEY 266
QY 217 QPQYVAFSVYILGTGTIGVAFNLV--VLRFTWNAEDEKRD-AEHRALLTRN 267
DB 267 LDFYKPVVMFWILVGLAYFAAVLSMIGDWLRVISKTKKEEVGEFRAHAAEWATAN 320
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Db 98 ELDELIQIIVAAINAGIIPLGNSNQSHWDLGSSFFAGTVITTTIGFNGISPRTEGGKI 157
QY 109 FCMFYALLIGIPLTLMVQFSLGERINTLVRYLLHRAKKGGMERRAD-----VSM 156
Db 158 FCIYVALLIGIPFGFLAGVGDQGTIF-----GKGIKVEDTTFIKMNVSTQTKIRI 208
QY 157 ANMVLIGFSCISTLCIGAAAFSHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQT 216
Db 209 ISTIIFILGCVLFVALPAVFKHIEGWSALDAIVFVVTITLTIGFDYVAGGSD--IEY 266
QY 217 QPQYVAFSVYILGTGTIGVAFNLV--VLRFTWNAEDEKRD-AEHRALLTRN 267
Db 267 LDFYKPVVMFWILVGLAYFAAVLSMIGDWLRVISKTKKEEVGEFRAHAAEWATAN 320

RESULT 9
US-09-336-643A-83
; Sequence 83, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PR1
; ORGANISM: H. sapiens
US-09-336-643A-83

Query Match      17.8%; Score 363; DB 3; Length 411;
Best Local Similarity 31.0%; Pred. No. 3.3e-31;
Matches 91; Conservative 59; Mismatches 102; Indels 42; Gaps 9;

QY 1 MKRQVRLALIVCTFTYLLVGAAYFVDALESEPELIERQRLERQELRARNLSQGGYE 60
DB 42 MKWKTGSTIFLVV--VLYLIIGAAVFKALEQOEISQRTTIVIQKTFISQHSVCNS--T 97
QY 61 ELERVVRL-KPHKAGV-----QWRPAGSFYFAITVITTYGHAAPSTDDGKV 108
DB 98 ELDELIQIIVAAINAGIIPLGNSNQSHWDLGSSFFAGTVITTTIGFNGISPRTEGGKI 157
QY 109 FCMFYALLIGIPLTLMVQFSLGERINTLVRYLLHRAKKGGMERRAD-----VSM 156
DB 158 FCIYVALLIGIPFGFLAGVGDQGTIF-----GKGIKVEDTTFIKMNVSTQTKIRI 208
QY 157 ANMVLIGFSCISTLCIGAAAFSHYEHWTFFQAYYCFITLTITIGFDYVALQKQALQT 216
DB 209 ISTIIFILGCVLFVALPAVFKHIEGWSALDAIVFVVTITLTIGFDYVAGGSD--IEY 266
QY 217 QPQYVAFSVYILGTGTIGVAFNLV--VLRFTWNAEDEKRD-AEHRALLTRN 267
DB 267 LDFYKPVVMFWILVGLAYFAAVLSMIGDWLRVISKTKKEEVGEFRAHAAEWATAN 320
```

```
RESULT 10
US-09-949-016-7001
; Sequence 7001, Application US/09949016
; Patent No. 6812339
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 07:58:54 ; Search time 101.398 Seconds
(without alignments)
1567.669 Million cell updates/sec

Title: US-09-503-089A-4
Perfect score: 2090
Sequence: 1 MAAPDLLDPKSAQNSKPL.....LNGLTPHCAGEDIAVIENMK 411

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2090	100.0	411	3	Aae10342 Murine TR
2	2084	99.7	411	2	Aay28497 Mouse h-T
3	2044	97.8	411	2	Aay34133 Human pot
4	2044	97.8	411	2	Aay28496 h-TREK1 p
5	2044	97.8	411	4	Aab50044 Human TRE
6	2044	97.8	411	7	Adp03586 Human GPC
7	2044	97.8	411	8	Adq76698 Human two
8	2041	97.7	411	3	Aae10341 Human TRE
9	2038	97.5	422	7	Adp03575 Human GPC
10	2033	97.3	411	5	Aae16597 Human TWI
11	2011	96.2	426	4	Aau07618 Human pot
12	2007	96.0	426	4	Aau07622 Human pot
13	2006	96.0	426	4	Aau07623 Human pot
14	2003	95.8	426	4	Aau07625 Human pot
15	2002	95.8	426	4	Aau07624 Human pot
16	1864	89.2	370	2	Aay30648 A mechani
17	1820.5	77.5	337	6	Abr41487 Human DIT
18	1251.5	59.9	538	5	Aab47930 Human TRE
19	1251.5	59.9	538	5	Aae16596 Human TWI
20	1251.5	59.9	538	5	Abp69333 Human pot
21	1251.5	59.9	543	5	Aae21804 Human TRE
22	1251.5	59.9	543	5	Aau81354 Novel hum
23	1251.5	59.9	543	5	Aau79472 Human nov
24	1251.5	59.9	543	5	Abb83542 Hypothala
25	1251.5	59.9	543	6	Ada05746 Human NOV

26	1251.5	59.9	543	7	AdR08315	Ade08315 Novel pro
27	1251.5	59.9	543	8	AdN62910	Adn62910 Human NOV
28	1247.5	59.7	543	5	AAU79473	Aau79473 Human nov
29	1224	58.6	724	5	AAO14193	Aao14193 Human tra
30	951	45.5	228	8	ADJ27190	Adj27190 Human TRI
31	797	38.1	392	6	ABU60891	Abu60891 Human G p
32	797	38.1	393	3	AAy94426	Aay94426 Human h-T
33	797	38.1	393	3	AAy94425	Aay94425 Human h-T
34	797	38.1	393	4	AAG67777	Aag67777 Human mec
35	797	38.1	419	5	AAG78406	Aag78406 Amino aci
36	797	38.1	419	7	Aae38597	Aae38597 Human pot
37	797	38.1	419	7	ADK52550	Adk52550 Hematolog
38	797	38.1	419	8	ADH51639	Adh51639 Human 123
39	797	38.1	419	8	ADI27936	Adi27936 Human TWI
40	797	38.1	419	8	ADR44894	Adr44894 Polypept1
41	797	38.1	1314	4	AAU04571	Aau04571 Human G-p
42	797	38.1	1314	6	ABU60872	Abu60872 Human G p
43	770.5	36.9	398	2	AAy30647	Aay30647 A mechani
44	762.5	36.5	398	5	AAE16598	Aae16598 Human TWI
45	635.5	30.4	383	4	ABG02731	Abg02731 Novel hum

ALIGNMENTS

RESULT 1
AAE10342
ID AAE10342 standard; protein; 411 AA.

AC AAE10342;

DT 10-DEC-2001 (first entry)

DE Murine TREK-1 potassium channel protein.

KW Murine; potassium channel protein; TREK-1; anaesthetic; analgesia; amnesia.

OS Mus musculus.

PN WO200047738-A2.

PD 17-AUG-2000.

PF 11-FEB-2000; 2000WO-IB000226.

PR 12-FEB-1999; 99US-0119727P.

PR 11-FEB-2000; 2000US-00503089.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;

XX WPI; 2000-549146/50.

XX N-PSDB; AAD17497.

XX Novel nucleic acid encoding a TREK-1 potassium channel protein for

XX transfecting cells to be used to identify compounds with anesthetic

XX properties.

XX Claim 9; Page 32-33; 39pp; English.

XX The invention relates to human and mouse TREK-1 potassium channel

XX proteins and their corresponding DNA molecules. TREK-1 nucleic acid is

XX useful for transfecting cells to induce expression of the TREK-1

XX potassium channel protein. These cells are then used in assays to

XX identify compounds which have anaesthetic properties, producing a safe,

XX reversible state of unconsciousness with concurrent amnesia and analgesia

XX in a mammal upon inhalation. The present sequence is murine TREK-1

XX potassium channel protein

XX Sequence 411 AA;

PT New nucleic acids encoding mammalian K-Hnov59 potassium channel proteins,
PT useful for the diagnosis and treatment of episodic ataxia with myokymia,
XX cardiac arrhythmia, epilepsy and Bartter's syndrome.

PS Claim 3; Page 104-105; 112pp; English.

XX This sequence represents the human K-Hnov59 potassium channel. K-Hnov
CC proteins have a high degree of homology to known potassium channels and
CC may be alpha subunits, which form the functional channel, or accessory
CC subunits that act to modulate the channel activity. K-Hnov59 is a 4
CC transmembrane domain, 2 pore domain potassium channel. The gene is
CC located on chromosome 19, determined via PCR chromosomal localisation
CC using primers AA211939 and AA211940. K-Hnov cDNAs were isolated by
CC extension of expressed sequence tags (ESTs) which were related but not
CC identical to known human potassium channels. Potential polymorphisms
CC detected as sequence variants between multiple independent clones.
CC Potassium channels have critical roles in various cell types and
CC biochemical pathways. Defective potassium channels are known to cause
CC four human diseases: episodic ataxia with myokymia; cardiac arrhythmia
CC (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium
CC channels are critical components of virtually all cells, it is likely
CC that abnormal potassium channels are also implicated in certain renal,
CC cardiovascular and central nervous system (CNS) disorders. Nucleotides
CC encoding K-Hnov proteins may be used for identifying homologous or
CC related proteins and the DNA sequences encoding them. They may be used to
CC produce compositions that modulate the expression and function of the
CC K-Hnov protein and in studying the biochemical pathways associated with
CC it. They may also be used for the recombinant production of K-Hnov
CC protein in fermentation cultures. Additionally, such nucleotides may be
CC used in gene therapy protocols for the treatment of diseases associated
CC with abnormal potassium channels

XX Sequence 411 AA;

Query Match 97.8%; Score 2044; DB 2; Length 411;

Best Local Similarity 96.4%; Pred. No. 3.5e-213; Indels 0; Gaps 0;

Matches 396; Conservative 11; Mismatches 4;

1 MAAPDLLDPKSAQAQSKPRLSFSTKPTVLASRVESDSTINVMKKTSTVIFLWVLYLII 60

1 MAAPDLLDPKSAQAQSKPRLSFSTKPTVLASRVESDSTINVMKKTSTVIFLWVLYLII 60

61 GAAVFKALPQOEISQRTTIVIKQTFIAQACVNSTELDELIQQIVAAINAGIPLGNS 120

61 GATVFKALPQOEISQRTTIVIKQTFISQHSVCVNSTELDELIQQIVAAINAGIPLGNT 120

121 SNQVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPFLGVLGAGVQ 180

121 SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPFLGVLGAGVQ 180

181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 240

181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 240

241 AIYFVVITLTITGFGDYVAGGSDIEYLDYFKPVVFWFLLVGLAYFAAVLSMIGDMLRVIS 300

241 AIYFVVITLTITGFGDYVAGGSDIEYLDYFKPVVFWFLLVGLAYFAAVLSMIGDMLRVIS 300

301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVIYDKFORATSVKTKLSAELAGNHQ 360

301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVIYDKFORATSVKTKLSAELAGNHQ 360

361 ELTPCRRTLTSVNHLTSEREVLPPLKABSIYINGLTPHCAGEDIAVIENMK 411

361 ELTPCRRTLTSVNHLTSEREVLPPLKABSIYINGLTPHCAGEDIAVIENK 411

RESULT 4

AAV28496

ID AAY28496 standard; protein; 411 AA.

XX

AC AAY28496;

XX

DT 12-OCT-1999 (first entry)

XX h-TREK1 polypeptide.

XX h-TREK1; two pore potassium channel; inflammatory disease;

XX chromosome 1q32.

XX Homo sapiens.

XX WO9937762-A1.

XX 29-JUL-1999.

XX 02-DEC-1998; 98WO-EP007805.

XX 27-JAN-1998; 98EP-00300570.

XX 09-OCT-1998; 98GB-00022135.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Meadows HJ, Chapman CG;

XX WPI: 1999-469126/39.

XX N-PSDB; AA200039.

XX New two pore potassium channel used for, e.g. treatment of cancer,

XX pulmonary, cardiovascular and inflammatory diseases.

XX Claim 3; Page 24; 44pp; English.

XX This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1

XX polynucleotide AA200039. h-TREK1 is a two pore potassium channel, and the

XX gene maps to human chromosome 1q32, between the markers DIS237 and

XX W15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a

XX disease or susceptibility to a disease related to expression or activity

XX of h-TREK1 polypeptides. The methods of diagnosis may be used in the

XX treatment of diseases including cancer, pulmonary, cardiovascular, and

XX inflammatory diseases, pain, psychiatric disorders including depression

XX and schizophrenia, neurodegenerative diseases including Alzheimer's,

XX stroke, and head trauma and neurological disorders including migraine.

XX Sequence 411 AA;

Query Match 97.8%; Score 2044; DB 2; Length 411;

Best Local Similarity 96.4%; Pred. No. 3.5e-213;

Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

1 MAAPDLLDPKSAQAQSKPRLSFSTKPTVLASRVESDSTINVMKKTSTVIFLWVLYLII 60

1 MAAPDLLDPKSAQAQSKPRLSFSTKPTVLASRVESDSTINVMKKTSTVIFLWVLYLII 60

61 GAAVFKALPQOEISQRTTIVIKQTFIAQACVNSTELDELIQQIVAAINAGIPLGNS 120

61 GATVFKALPQOEISQRTTIVIKQTFISQHSVCVNSTELDELIQQIVAAINAGIPLGNT 120

121 SNQVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPFLGVLGAGVQ 180

121 SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPFLGVLGAGVQ 180

181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 240

181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 240

241 AIYFVVITLTITGFGDYVAGGSDIEYLDYFKPVVFWFLLVGLAYFAAVLSMIGDMLRVIS 300

241 AIYFVVITLTITGFGDYVAGGSDIEYLDYFKPVVFWFLLVGLAYFAAVLSMIGDMLRVIS 300

301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVIYDKFORATSVKTKLSAELAGNHQ 360

301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRRLSVIYDKFORATSVKTKLSAELAGNHQ 360

361 ELTPCRRTLTSVNHLTSEREVLPPLKABSIYINGLTPHCAGEDIAVIENMK 411

361 ELTPCRRTLTSVNHLTSEREVLPPLKABSIYINGLTPHCAGEDIAVIENK 411

Db 361 ELTPCRRTLSVNHLSERDVLPLPKTESIYLNGLTPHCAGEIAVIENIK 411

RESULT 5

AA050044

ID AAB50044 standard; protein; 411 AA.

AC AAB50044;

XX 19-MAR-2001 (first entry)

DT 19-MAR-2001 (first entry)

XX Human TREK.

DE Human; TREK; 2P domain potassium channel; resting membrane potential; neuronal excitability; neurotransmitter release modulation; epilepsy; neurological disorder; sleep-related disorder; cognitive dysfunction; attention deficit disorder; addiction; anxiety; phobia; Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence; erectile dysfunction; alopecia.

KW Homo sapiens.

OS WO200072863-A2.

PN 07-DEC-2000.

PD 01-JUN-2000; 2000WO-CB002107.

XX 01-JUN-1999; 99GB-00012733.

PR (SMIK) SMITHKLINE BEECHAM PLC.

PA Hervieu GJ, Meadows HJ, Randall AD;

PI WPI; 2001-080422/09.

XX N-PSDB; AAC90412.

DR Use of human TREK1 polypeptide, polynucleotides encoding them and modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related disorders, addition and dyskinesias including Parkinson's and Huntington's chorea.

XX Claim 7; Page 29; 35pp; English.

CC The present sequence is human TREK1 (h-TREK1). h-TREK1 is a member of the 2P domain potassium channel family of proteins which play a part in the control of resting membrane potential. Modulation of these channels will therefore affect neuronal excitability, thereby leading to a modulation of neurotransmitter release and activity of neuronal networks. Such modulation therefore may be useful for the treatment of certain neurological conditions such as epilepsy, sleep-related disorders, cognitive dysfunction, attention deficit disorder, addiction, anxiety/phobia, Parkinson's and Huntington's chorea, cerebral palsy, incontinence, erectile dysfunction or alopecia

XX Sequence 411 AA;

SQ Query Match 97.8%; Score 2044; DB 4; Length 411; Best Local Similarity 96.4%; Pred. No. 3.5e-213; Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAAPDLDPKSAQNSKPLSPSSKPTVLASRVSDSAINVMKKTSTFIPLVVLII 60

Db 1 MAAPDLDPKSAQNSKPLSPSTPTVLASRVSDSTTINVMKKTSTFIPLVVLII 60

Qy 61 GAAVFKALPQPOEISORTTIVIKQTFIAQACVNSTELDELIQIVAAINAGIIPLGNS 120

Db 61 GATVFKALPQPEIHSORTTIVIKQTFISQHSVNSTELDELIQIVAAINAGIIPLGNT 120

Qy 121 SNQVSHWDLGSSFFAGTVITTTIGFNGISPRTEGGKIFCIIVALLGIPFLPGVGDQ 180

Db 121 SNQISHWDLGSSFFAGTVITTTIGFNGISPRTEGGKIFCIIVALLGIPFLPGVGDQ 180

Qy 181 LGTIFGKGIKVEDTFIKWNVSTQKIRIISTIIIFILGCVLFLVALPAVIFKHIEGWSALD 240

Db 181 LGTIFGKGIKVEDTFIKWNVSTQKIRIISTIIIFILGCVLFLVALPAVIFKHIEGWSALD 240

Qy 241 AIYFWVITLTITIGFDYVAGSDIEYLDYFYPVWFWILVGLAYFAAVLSMIGDWLRVIS 300

Db 241 AIYFWVITLTITIGFDYVAGSDIEYLDYFYPVWFWILVGLAYFAAVLSMIGDWLRVIS 300

Qy 301 KKTKEEVGEPFAHAAEWNTAVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360

Db 301 KKTKEEVGEPFAHAAEWNTAVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360

Qy 361 ELTPCRRTLSVNHLSERDVLPLPKTESIYLNGLTPHCAGEIAVIENIK 411

Db 361 ELTPCRRTLSVNHLSERDVLPLPKTESIYLNGLTPHCAGEIAVIENIK 411

RESULT 6

ADP03586

ID ADP03586 standard; protein; 411 AA.

XX ADP03586;

AC ADP03586;

XX 29-JUL-2004 (first entry)

DT 29-JUL-2004 (first entry)

XX Human GPCR potassium channel, subfamily K, member 2 protein.

DE GPCR; G-protein coupled receptor; neuroprotective; nootropic; tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant; anticonvulsant; antiparkinsonian; cytotostatic; cardiac; hypotensive; antianginal; analgesic; anorectic; anti-HIV; antiasthmatic; osteopathic; uropathic; antiulcer; antiallergic; cell cycle regulation; neurological; severe mental retardation; dyskinesia; brain; spinal cord; affective; neoplastic; cardiovascular; immunological; immune; endocrinal; growth; eating; HIV infection; cancer; metabolic; pituitary; chromosome identification; gene therapy; human; receptor; potassium channel subfamily K member 2.

KW Homo sapiens.

OS WO20003062393-A2.

PN 31-JUL-2003.

PD 22-JAN-2003; 2003WO-US001911.

XX 22-JAN-2002; 2002US-0350724P.

PR (BRIM) BRISTOL-MYERS SQUIBB CO.

PA Ramanathan CS, Gopal S, Mintier G, Feder JN;

PI WPI; 2003-618283/58.

XX New nucleic acid molecule encoding a human G-protein coupled receptor, useful for diagnosing, preventing or treating diseases involving the receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or cancer.

PT Example 1; SEQ ID NO 31; 224pp; English.

PS The invention relates to a novel isolated GPCR (G-protein coupled receptor) nucleic acid molecule. The polynucleotide and polypeptide of the invention demonstrate neuroprotective, nootropic, tranquiliser, antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant, antiparkinsonian, cytotostatic, cardiac, hypotensive, antianginal, analgesic, anorectic, anti-HIV, antiasthmatic, osteopathic, uropathic, antiulcer and antiallergic properties. The nucleic acid molecule and polypeptide of the invention may be useful in diagnosing, preventing, treating or ameliorating a medical condition, such as a disorder related to aberrant G-protein coupled signalling, a disorder related to aberrant cell cycle regulation, neurological disorders, severe mental retardation and dyskinesias, brain disorders, spinal cord disorders, affective

CC disorders, neoplastic disorders, cardiovascular disorders, immunological
 CC disorders, immune-related disorders, endocrinal diseases, growth
 CC disorders, eating disorders, HIV infection, cancers, metabolic disorders
 CC and pituitary disorders. Furthermore, the polynucleotide may be used in
 CC chromosome identification, in identifying organisms from minute
 CC biological samples, in gene therapy or as a molecular weight marker. The
 CC current sequence is that of a human GPCR (G-protein coupled receptor)
 CC protein of the invention which was used for homology purposes.

XX Sequence 411 AA;

Query Match 97.8%; Score 2044; DB 7; Length 411;
 Best Local Similarity 96.4%; Pred. No. 3.5e-213;
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKTKVSTIFLVVLYLII 60
 DB 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKTKVSTIFLVVLYLII 60

QY 61 GAAVFKALEQPOEISORTTIVIQKQTFIAQAHACVNSTELDELIQQIVAAINAGIIPLGNT 120
 DB 61 GATVFKALEQPEHISORTTIVIQKQTFISQHSVCVNSTELDELIQQIVAAINAGIIPLGNT 120

QY 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDO 180
 DB 121 SNOISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDO 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHEGWSALD 240
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHEGWSALD 240

QY 241 AIYFVVITLTITIGFGDYVAGGSDIEYLDYFKPVPVFWILVGLAYFAAVLSMIGDMLRVIS 300
 DB 241 AIYFVVITLTITIGFGDYVAGGSDIEYLDYFKPVPVFWILVGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRKLSAELAGNHQ 360
 DB 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRKLSAELAGNHQ 360

QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 411
 DB 361 ELTPCRRTLNVNHLTSERDVLPLPKTESIYLNGLTPHCAGEIAVIENIK 411

RESULT 7

ADQ76698
 ID ADQ76698 standard; protein; 411 AA.

AC ADQ76698;

DT 07-OCT-2004 (first entry)

DE Human two pore domain potassium channel TREK-1.

XX TREK-1; sleep; two pore domain potassium channel; sedative; hypnotic;
 KW human.

OS Homo sapiens.

XX WO2004058325-A2.

PN 15-JUL-2004.

XX 23-DEC-2003; 2003WO-US040913.

XX 23-DEC-2002; 2002US-0436201P.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX Tononi G, Cirelli C;

XX WPI; 2004-534024/51.

DR GENBANK; NM014217.

XX

PT Identifying a Drosophila mutant fly with a no rebound, short sleep and/or
 no sleep deprivation resistant phenotype, for identifying sleep-related
 molecular targets, comprises recording sleep quantity of the mutant fly.

PS Claim 12; SEQ ID NO 2; 83pp; English.

XX The present sequence is that of the human two pore domain K⁺ channel TREK
 -1. In rats, TREK-1 is highly expressed in much of the brain and is
 inhibited by protein kinase C and protein kinase C mediated
 phosphorylation. It is activated by volatile general anaesthetics and is
 expressed at high levels in the brain of sleep animals. Based on these
 criteria and on experimental results, it is hypothesized that TREK-1 is a
 key mediator of sleep (when open) and waking (when closed). The invention
 provides methods for identifying a sleep- or wakefulness-promoting
 compound based on the compound's ability to modulate two pore domain K⁺
 channels such as TREK-1. It also provides screening methods for isolating
 short sleep, no rebound and sleep deprivation resistant Drosophila
 mutants useful for identifying sleep-related molecular targets.

XX Sequence 411 AA;

Query Match 97.8%; Score 2044; DB 8; Length 411;
 Best Local Similarity 96.4%; Pred. No. 3.5e-213;
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKTKVSTIFLVVLYLII 60

DB 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKTKVSTIFLVVLYLII 60

QY 61 GAAVFKALEQPOEISORTTIVIQKQTFIAQAHACVNSTELDELIQQIVAAINAGIIPLGNS 120

DB 61 GATVFKALEQPEHISORTTIVIQKQTFISQHSVCVNSTELDELIQQIVAAINAGIIPLGNT 120

QY 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDO 180

DB 121 SNOISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDO 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHEGWSALD 240

DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHEGWSALD 240

QY 241 AIYFVVITLTITIGFGDYVAGGSDIEYLDYFKPVPVFWILVGLAYFAAVLSMIGDMLRVIS 300

DB 241 AIYFVVITLTITIGFGDYVAGGSDIEYLDYFKPVPVFWILVGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRKLSAELAGNHQ 360

DB 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRKLSAELAGNHQ 360

QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 411

DB 361 ELTPCRRTLNVNHLTSERDVLPLPKTESIYLNGLTPHCAGEIAVIENIK 411

RESULT 8

AAE10341

ID AAE10341 standard; protein; 411 AA.

XX AAE10341;

AC AAE10341;

DT 10-DEC-2001 (first entry)

XX Human TREK-1 potassium channel protein.

XX Human; potassium channel protein; TREK-1; anaesthetic; analgesia;
 KW amnesia.

XX Homo sapiens.

XX WO200047738-A2.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-IB000226.
 PF
 XX
 PR 12-FEB-1999; 99US-0119727P.
 PR 11-FEB-2000; 2000US-00503089.
 XX
 XX (CNRS) CNRS CENT NAT RECH SCI.
 PA
 XX
 XX Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;
 FI
 XX WPI; 2000-549146/50.
 DR N-PSDB; AAD17496.
 DR
 XX
 XX Novel nucleic acid encoding a TREK-1 potassium channel protein for
 PT transfecting cells to be used to identify compounds with anesthetic
 PT properties.
 XX
 XX Claim 3; Page 28; 39pp; English.
 PS
 XX The invention relates to human and mouse TREK-1 potassium channel
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
 CC useful for transfecting cells to induce expression of the TREK-1
 CC potassium channel protein. These cells are then used in assays to
 CC identify compounds which have anaesthetic properties, producing a safe,
 CC reversible state of unconsciousness with concurrent amnesia and analgesia
 CC in a mammal upon inhalation. The present sequence is human TREK-1
 CC potassium channel protein
 CC
 XX Sequence 411 AA;
 SQ
 Query Match 97.7%; Score 2041; DB 3; Length 411;
 Best Local Similarity 96.1%; Pred. No. 7.5e-213;
 Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTFIPLVVLYLII 60
 DB 1 MAAPDLLDPKSAQNSKPRLSFSTPTVLASRVESDTINVMKWTSTFIPLVVLYLII 60
 QY 61 GAAVFKALEQPOEISORTTIVIQKTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120
 DB 61 GATVFKALEQPOEISORTTIVIQKTFISQHCNVNSTELDELIQOIVAAINAGIPLGNT 120
 QY 121 SNOVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIVALLGIFLFGFLLAGVGQ 180
 DB 121 SNOVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIVALLGIFLFGFLLAGVGQ 180
 QY 181 LGTIFGKIAKVEDFIKWNVSQTKIRIISTITIFLFGCVLFVALPVAIFKHIEGWSALD 240
 DB 181 LGTIFGKIAKVEDFIKWNVSQTKIRIISTITIFLFGCVLFVALPVAIFKHIEGWSALD 240
 QY 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVVFWFVLVGLAYFAAIVLSMIGDWLRVTS 300
 DB 241 AIYFVVITLTITGFGDYVAGSDIEYLDYKPVVFWFVLVGLAYFAAIVLSMIGDWLRVTS 300
 QY 301 KKTKEEVGFRAHAETANVTAEFKETRRRLSVEIYDKFORATSVKRLSIAELAGNHQ 360
 DB 301 KKTKEEVGFRAHAETANVTAEFKETRRRLSVEIYDKFORATSVKRLSIAELAGNHQ 360
 QY 361 ELTPCRRLTSVNLHLSERVLPLLKAESIYLNGLTTPHCAGRDIAVIENMK 411
 DB 361 ELTPCRRLTSVNLHLSERVLPLLKATESIYLNGLTTPHCAGEIAVIENIK 411
 RESULT 9
 ADP03575
 ID ADP03575 standard; protein; 422 AA.
 XX
 AC ADP03575;
 XX
 XX 29-JUL-2004 (first entry)
 DT Human GPCR twin pore channel" protein variant "Gene 9" protein.
 XX
 DE
 XX

KW GPCR; G-protein coupled receptor; neuroprotective; nootropic;
 KW tranquilizer; antimigraine; neuroleptic; antimanic; antidepressant;
 KW anticonvulsant; antiparkinsonian; cytostatic; cardiant; hypotensive;
 KW antianalgesic; anorectic; anti-HIV; antisthmatic; osteopathic;
 KW uropathic; antitumor; antiallergic; cell cycle regulation; neurological;
 KW severe mental retardation; dyskinesia; brain; spinal cord; affective;
 KW neoplastic; cardiovascular; immunological; immune; endocrinal; growth;
 KW eating; HIV infection; cancer; metabolic; pituitary;
 KW chromosome identification; gene therapy; human; receptor;
 KW twin pore channel; potassium channel subfamily K member 2 variant.
 XX Homo sapiens.
 XX
 XX WO2003062393-A2.
 XX 31-JUL-2003.
 XX
 XX 22-JAN-2003; 2003WO-US001911.
 XX
 XX 22-JAN-2002; 2002US-0350724P.
 XX (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX Ramanathan CS, Gopal S, Mintier G, Feder JN;
 PI WPI; 2003-618283/58.
 DR N-PSDB; ADP03564.
 DR
 XX New nucleic acid molecule encoding a human G-protein coupled receptor,
 PT useful for diagnosing, preventing or treating diseases involving the
 PT receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
 PT cancer.
 XX
 PS Claim 5; SEQ ID NO 20; 224pp; English.
 XX The invention relates to a novel isolated GPCR (G-protein coupled
 CC receptor) nucleic acid molecule. The polynucleotide and polypeptide of
 CC the invention demonstrate neuroprotective, nootropic, tranquilizer,
 CC antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,
 CC analgesic, anorectic, anti-HIV, antisthmatic, osteopathic, uropathic,
 CC antitumor and antiallergic properties. The nucleic acid molecule and
 CC polypeptide of the invention may be useful in diagnosing, preventing,
 CC treating or ameliorating a medical condition, such as a disorder related
 CC to aberrant G-protein coupled signalling, a disorder related to aberrant
 CC cell cycle regulation, neurological disorders, severe mental retardation
 CC and dyskinesias, brain disorders, spinal cord disorders, affective
 CC disorders, neoplastic disorders, cardiovascular disorders, growth
 CC disorders, immune-related disorders, endocrinal diseases, growth
 CC disorders, eating disorders, HIV infection, cancers, metabolic disorders
 CC and pituitary disorders. Furthermore, the polynucleotide may be used in
 CC chromosome identification, in identifying organisms from minute
 CC biological samples, in gene therapy or as a molecular weight marker. The
 CC current sequence is that of a human GPCR (G-protein coupled receptor)
 CC protein which was isolated by the method of the invention.
 XX
 SQ Sequence 422 AA;
 Query Match 97.5%; Score 2038; DB 7; Length 422;
 Best Local Similarity 95.9%; Pred. No. 1.7e-212;
 Matches 394; Conservative 13; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTFIPLVVLYLII 60
 DB 12 LAAPDLLDPKSAQNSKPRLSFSTPTVLASRVESDTINVMKWTSTFIPLVVLYLII 71
 QY 61 GAAVFKALEQPOEISORTTIVIQKTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120
 DB 72 GATVFKALEQPOEISORTTIVIQKTFISQHCNVNSTELDELIQOIVAAINAGIPLGNT 131
 QY 121 SNOVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIVALLGIFLFGFLLAGVGQ 180
 DB 132 SNOVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIVALLGIFLFGFLLAGVGQ 191

QY 181 LGTIFGKGIKVEDTPIKWNVSOTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
 DB 192 LGTIFGKGIKVEDTPIKWNVSOTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 251
 QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300
 DB 252 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 311
 QY 301 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRLSIAELAGNHQ 360
 DB 312 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRLSIAELAGNHQ 371
 QY 361 ELTPCRTLTVNHLTSERVLPPLLKAESIYLNGLTPHCAGEDIAVIENWK 411
 DB 372 ELTPCRTLTVNHLTSERDVLPPLLKTESIYLNGLTPHCAGEDIAVIENIK 422

RESULT 10

AAE16597
 ID AAE16597 standard; protein; 411 AA.

XX AC AAE16597;

DT 18-APR-2002 (first entry)

XX Human TWIK-Related K+ Channel-1 (TREK-1) protein.

DE Human TWIK-Related K+ Channel-1; TREK-1; anaesthetic; screening.

KW Human; TWIK-Related K+ Channel-1; TREK-1; anaesthetic; screening.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Region 47..65
 FT Domain /note= "M1 membrane spanning segment"
 FT Domain 127..150
 FT Region /note= "P1 pore domain"
 FT Region 158..178
 FT Region /note= "M2 membrane spanning segment"
 FT Region 209..230
 FT Domain /note= "M3 membrane spanning segment"
 FT Domain 236..259
 FT Region /note= "P2 pore domain"
 FT Region 274..293
 FT Domain /note= "M4 membrane spanning segment"

XX WO200200715-A2.

XX 03-JAN-2002.

XX 27-JUN-2001; 2001WO-IB001436.

XX 27-JUN-2000; 2000US-0214559P.

XX 27-JUN-2001; 2001US-00892360.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lesage F, Romey G;

XX WPI; 2002-139903/18.

XX New mammalian K+ channel protein with two pore domains, for screening
 PT various compounds, particularly for identifying biologically active
 PT compounds with anaesthetic properties.

XX Disclosure; Fig 1A; 50pp; English.

XX The invention relates to a mammalian K+ channel protein with two pore
 CC domains, called TREK2 (TWIK-Related K+ Channel). The protein produces
 CC currents whose current-voltage relationship is slightly inwardly
 CC rectifying in high symmetrical K+ conditions. TREK2 is a member of the
 CC fatty acid-activated and mechanosensitive K+ channel family. TREK-2 gene
 CC located on chromosome 14q31 is abundantly expressed in kidney, pancreas

CC and moderately in testis, brain, colon and small intestine. The mammalian
 CC K+ channel protein is useful in methods for screening various compounds.
 CC In particular, the protein is useful in methods for identifying
 CC biologically active compounds with anaesthetic properties. The present
 CC sequence is TREK-1 protein used in the invention

XX Sequence 411 AA;

Query Match 97.3%; Score 2033; DB 5; Length 411;
 Best Local Similarity 95.9%; Pred. No. 5.6e-212;
 Matches 394; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPLSPSSKPTVLASRVESDAINVMKWTSTIFLVVLLII 60
 DB 1 MAAPDLLDPKSAQNSKPLSPSSKPTVLASRVESDAINVMKWTSTIFLVVLLII 60
 QY 61 GAAVFKALEQPOBISORTTIVIKQTFIAQACVNSTELDELIIQIVAAINAGIIPLGNS 120
 DB 61 GATVFKALEQPOBISORTTIVIKQTFIAQACVNSTELDELIIQIVAAINAGIIPLGNT 120
 QY 121 SNQVSHWDLGSSFFPAGTVITTTIGFNIISPTREGGKIFCIIYALLGIPFGFLLAGVDQ 180
 DB 121 SNQVSHWDLGSSFFPAGTVITTTIGFNIISPTREGGKIFCIIYALLGIPFGFLLAGVDQ 180
 QY 181 LGTIFGKGIKVEDTPIKWNVSOTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
 DB 181 LGTIFGKGIKVEDTPIKWNVSOTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
 QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300
 DB 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDWLRVIS 300
 QY 301 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRLSIAELAGNHQ 360
 DB 301 KKTKEEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFQRATSVKRLSIAELAGNHQ 360
 QY 361 ELTPCRTLTVNHLTSERVLPPLLKAESIYLNGLTPHCAGEDIAVIENWK 411
 DB 361 ELTPCRTLTVNHLTSERDVLPPLLKTESIYLNGLTPHCAGEDIAVIENIK 411

RESULT 11

AAU07618
 ID AAU07618 standard; protein; 426 AA.

XX AC AAU07618;

XX 21-NOV-2001 (first entry)

XX Human potassium ion channel TPKC1 protein.

XX Transmembrane potassium ion channel protein; inward potassium flux;
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;
 KW insect; TPKC1; human.

XX Homo sapiens.

XX WO200161006-A2.

XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004680.

XX 15-FEB-2000; 2000US-00503849.

XX (BADI) BASF CORP.

XX Pausch MH;

XX WPI; 2001-536570/59.

XX N-PSDB; AAS12169.

XX New polypeptide, a mutant potassium ion channel protein for improving

Db 76 GATVFKALEQPHIEISQRTTIVIQKTFISQHSVCNVSTELDELIQQIVAAINAGIPLGNT 135
Qy 121 SNQVSHWDLGSSFFAGVTITIGFNIISPRTEGGKIFCIIVALLGIFLFGFLAGVGDO 180
Db 136 SNQVSHWDLGSSFFAGVTITIGFNIISPRTEGGKIFCIIVALLGIFLFGFLAGVGDO 195
Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 255
Qy 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVLSMIGDLVRVIS 300
Db 256 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVLSMIGDLVRVIS 315
Qy 301 KKTKEEVGEFRAHAAEWNTAVTAEFKTRRLSVIEYDKFORATSVKRLSAELAGNHQ 360
Db 316 KKTKEEVGEFRAHAAEWNTAVTAEFKTRRLSVIEYDKFORATSVKRLSAELAGNHQ 375
Qy 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411
Db 376 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENIK 426

RESULT 15

AAU07624
ID AAU07624 standard; protein; 426 AA.

XX AAU07624;

XX 21-NOV-2001 (first entry)

XX Human potassium ion channel TPKC1 mutant protein #3.

XX Transmembrane potassium ion channel protein; inward potassium flux;
KW pest control; membrane potential; pesticide; antihelminthic; nematode;
KW insect; TPKC1; human; mutant; mutein.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 272
/note= "Wild-type Tyr replaced by His"

FT Misc-difference 274
/note= "Wild-type Ala replace by Val"

XX WO200161006-A2.

XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004680.

XX 15-FEB-2000; 2000US-00503849.

XX (BADI) BASF CORP.

XX Pausch MH;

XX WPI; 2001-536570/59.

XX N-PSDB; AAS12183.

XX New polypeptide, a mutant potassium ion channel protein for improving
inward potassium flux under acidic conditions.

XX Claim 37; Page 117-119; 131pp; English.

XX The invention relates to a mutant potassium ion channel protein, having
four membrane spanning domains and two pore forming domains, comprising a
mutation at the second pore forming domain. The expression of the mutant
protein in a cell confers improved inward potassium flux and the ability
to grow in the presence of potassium. Mutant proteins and their
corresponding polynucleotide sequences can therefore be used to improve
inward potassium flux into cells under acidic conditions by modulating
the membrane potential using therapeutic agents. The sequences may be

CC used to develop agonists and antagonists of potassium channel proteins in
order to control pests such as nematodes and insects. This sequence
CC represents a human transmembrane potassium ion channel TPKC1 mutant
protein

XX Sequence 426 AA;

Query Match 95.8%; Score 2002; DB 4; Length 426;

Best Local Similarity 94.6%; Pred. No. 1.4e-208;

Matches 389; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MAAPDLLDPKSAQAQNSKPRLSFSKPTVLAGRVSDSAINVMKMTVSTIFLVVLYLII 60

Db 16 VAAPDLLDPKSAQAQNSKPRLSFSKPTVLAGRVSDTTINVMKMTVSTIFLVVLYLII 75

Qy 61 GAAVFKALEQPHIEISQRTTIVIQKTFIAQACNVSTELDELIQQIVAAINAGIPLGNS 120

Db 76 GATVFKALEQPHIEISQRTTIVIQKTFISQHSVCNVSTELDELIQQIVAAINAGIPLGNT 135

Qy 121 SNQVSHWDLGSSFFAGVTITIGFNIISPRTEGGKIFCIIVALLGIFLFGFLAGVGDO 180

Db 136 SNQVSHWDLGSSFFAGVTITIGFNIISPRTEGGKIFCIIVALLGIFLFGFLAGVGDO 195

Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 255

Qy 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVLSMIGDLVRVIS 300

Db 256 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVLSMIGDLVRVIS 315

Qy 301 KKTKEEVGEFRAHAAEWNTAVTAEFKTRRLSVIEYDKFORATSVKRLSAELAGNHQ 360

Db 316 KKTKEEVGEFRAHAAEWNTAVTAEFKTRRLSVIEYDKFORATSVKRLSAELAGNHQ 375

Qy 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411

Db 376 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENIK 426

Search completed: July 13, 2005, 08:39:47

Job time : 102.398 secs

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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:01:55 ; Search time 93.9622 Seconds
(without alignments)
2239.886 Million cell updates/sec

Title: US-09-503-089A-4
Perfect score: 2090
Sequence: 1 MAAPDLLDPKSAQNSKPKL.....LNGLTPHCAGEDIAVIENMK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2090	100.0	411	1 CIW2_MOUSE	P97438 mus musculu
2	2082	99.6	414	2 Q6P6P9	Q6P6P9 mus musculu
3	2061	98.6	426	2 Q920B6	Q920B6 rattus norv
4	2044	97.8	411	2 Q9NRT2	Q9NRT2 homo sapien
5	2034	97.3	411	2 Q8HY88	Q8HY88 bos taurus
6	2011	96.2	426	1 CIW2_HUMAN	Q95069 homo sapien
7	1261.5	60.4	538	2 Q6Q834	Q6Q834 oryctolagus
8	1256.5	60.1	453	2 Q8B2B0	Q8B2B0 m mus muscu
9	1256.5	60.1	535	2 Q8BUW1	Q8BUW1 m mus muscu
10	1256.5	60.1	538	1 CIWA_RAT	Q91184 rattus norv
11	1251.5	59.9	538	1 CIWA_HUMAN	P57789 homo sapien
12	1251.5	59.9	543	2 Q6B0I4	Q6B0I4 homo sapien
13	1223.5	58.5	546	2 Q68EY1	Q68EY1 xenopus lae
14	797	38.1	393	1 CIW4_HUMAN	Q9NYG8 homo sapien
15	770.5	36.9	398	1 CIW4_MOUSE	Q88454 mus musculu
16	757.5	36.2	397	2 Q924I4	Q924I4 rattus norv
17	624	29.9	241	2 Q9CX88	Q9CX88 m mus muscu
18	499.5	23.9	309	1 CIW6_HUMAN	Q96T55 homo sapien
19	493.5	23.6	294	2 Q6X6Z5	Q6X6Z5 homo sapien
20	482.5	23.1	152	2 Q6ZW95	Q6ZW95 homo sapien
21	453	21.7	262	2 Q6X6Z3	Q6X6Z3 homo sapien
22	447	21.4	322	2 Q6X6Z4	Q6X6Z4 homo sapien
23	434.5	20.8	448	2 Q6PFU3	Q6PFU3 brachydanio
24	420	20.1	499	1 CIW5_HUMAN	Q95279 homo sapien
25	409	19.6	502	2 Q9JK62	Q9JK62 m potassium
26	404	19.3	341	2 Q8HZT2	Q8HZT2 bos taurus
27	403.5	19.3	257	2 Q80XE0	Q80XE0 mus musculu
28	402.5	19.3	307	2 Q80IT4	Q80IT4 xenopus lae
29	395	18.9	184	2 Q8N4V5	Q8N4V5 homo sapien
30	389	18.6	332	1 CIW8_HUMAN	Q96T54 homo sapien
31	377	18.0	336	2 Q8R454	Q8R454 cavia porce

32	377	18.0	336	2 Q99L99	Q99L99 mus musculu
33	376.5	18.0	336	1 CIW1_HUMAN	Q00180 homo sapien
34	375.5	18.0	336	2 Q922T2	Q922T2 rattus norv
35	370	17.7	336	1 CIW1_MOUSE	Q08581 mus musculu
36	370	17.7	336	1 CIW3_HUMAN	O14649 homo sapien
37	364.5	17.4	331	2 Q8AVI5	Q8AVI5 xenopus lae
38	353.5	16.9	259	2 Q02821	Q02821 oryctolagus
39	351.5	16.8	330	1 CIWF_HUMAN	Q9H427 homo sapien
40	351.5	16.8	365	1 CIW9_CAVPO	Q9J158 cavia porce
41	351	16.8	323	2 Q6PEI1	Q6PEI1 brachydanio
42	351	16.8	409	1 CIW3_MOUSE	Q35111 mus musculu
43	351	16.8	411	1 CIW3_RAT	O54912 rattus norv
44	346.5	16.6	374	2 Q63ZIO	Q63ZIO xenopus lae
45	345.5	16.5	396	2 Q923V6	Q923V6 rattus norv

ALIGNMENTS

RESULT 1

CIW2_MOUSE

ID CIW2_MOUSE STANDARD; PRT; 411 AA.

AC P97438;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 2 (Outward rectifying potassium

DE channel protein TREK-1) (Two-pore potassium channel TPKC1) (TREK-1 K+

DE channel subunit).

GN Name=Kcnk2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.

RC TISSUE=Brain;

RX MEDLINE=97157476; PubMed=9003761;

RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,

RA Lazdunski M.;

RT "Cloning, functional expression and brain localization of a novel

RT unconventional outward rectifier K+ channel.";

RL EMBO J. 15:6854-6862(1996).

RN [2]

RP REVISIONS.

RC TISSUE=Brain;

RA Fink M., Duprat F., Lesage F., Reyes R., Romey G., Heurteaux C.,

RA Lazdunski M.;

RP Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RP ACTIVATION.

RX MEDLINE=99254548; PubMed=1031245; DOI=10.1038/8084;

RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;

RT "Inhalational anesthetics activate two-pore-domain background K+

RT channels.";

RL Nat. Neurosci. 2:422-426(1999).

CC -!- FUNCTION: Outward rectifying potassium channel.

CC -!- SUBUNIT: Homodimer (Potential).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: High expression in brain and lung. Also

CC detected in kidney, heart and skeletal muscle. Not detected in

CC liver. In the brain, highest expression in olfactory bulb,

CC hippocampus and cerebellum.

CC -!- MISCELLANEOUS: Inhibited by barium. Activated by volatile general

CC anaesthetics such as chloroform, diethyl ether, halothane and

CC isoflurane.

CC -!- SIMILARITY: Belongs to the two pore domain potassium channel

CC (TC 1.A.1.8) family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; U73488; AAC53005.2; -;
DR MGD; MGI:109366; Kcnk2.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IDA.
DR GO; GO:0006813; P:potassium ion transport; IDA.
DR InterPro; IPR003280; K+channel 2pore.
DR InterPro; IPR001622; K+channel 2pore.
DR InterPro; IPR003976; Trek channel.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
DR Glycoprotein; Ion transport; Ionic channel; Potassium;
KW Potassium channel; Transmembrane; Transport; Voltage-gated channel.
FT DOMAIN 1 46 Cytoplasmic (Potential).
FT TRANSMEM 47 67 Potential.
FT DOMAIN 129 155 Pore-forming 1 (Potential).
FT TRANSMEM 157 177 Potential.
FT DOMAIN 178 207 Cytoplasmic (Potential).
FT TRANSMEM 208 228 Potential.
FT DOMAIN 238 268 Pore-forming 2 (Potential).
FT TRANSMEM 273 293 Potential.
FT DOMAIN 294 411 Cytoplasmic (Potential).
FT DOMAIN 378 411 Essential for chloroform and haloethane sensitivity.
FT DOMAIN 354 411 Required for basal channel activity.
FT CARBOHYD 95 95 N-linked (GlcNAc. . .) (Potential).
FT CARBOHYD 119 119 N-linked (GlcNAc. . .) (Potential).
SQ SEQUENCE 411 AA; 45297 MW; 8F976DDD103EFA05 CRC64;

Query Match 100.0%; Score 2090; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 4.3e-133; Mismatches 0; Indels 0; Gaps 0;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLII 60
QY 61 GAAVFKALEQPEQISQRTTIVIQKTFIAQHACVNSTELDELIQIIVAAINAGIIPLGNS 120
DB 61 GAAVFKALEQPEQISQRTTIVIQKTFIAQHACVNSTELDELIQIIVAAINAGIIPLGNS 120
QY 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIYALLGIFLPGFLAGVGQ 180
DB 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIYALLGIFLPGFLAGVGQ 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 240
DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 240
QY 241 AIYFVVITLTITGFDYVAGGSDIEYDFYKPVVFWLVLGAYFAAVLSMTGDLWRVIS 300
DB 241 AIYFVVITLTITGFDYVAGGSDIEYDFYKPVVFWLVLGAYFAAVLSMTGDLWRVIS 300
QY 301 KTKKEVGFRAHAETANTVAETKTRRLSVIYDKFQATSVKRLSIAELAGNHQ 360
DB 301 KTKKEVGFRAHAETANTVAETKTRRLSVIYDKFQATSVKRLSIAELAGNHQ 360
QY 361 ELTPCRRTLNVNHLISEREVLPLKAEISYINGLTPHCAGEDIAVIENMK 411
DB 361 ELTPCRRTLNVNHLISEREVLPLKAEISYINGLTPHCAGEDIAVIENMK 411

RESULT 2
Q6P6P9
ID Q6P6P9 PRELIMINARY; PRT; 414 AA.
AC Q6P6P9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Kcnk2 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences".
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
(TC 1.A.1.8) family.
CC EMBL; BC062094; AAHG2094.1; -;
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.
DR GO; GO:0005249; F:voltage-gated potassium channel activity; IDA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IDA.
DR GO; GO:0006813; P:potassium ion transport; IDA.
DR InterPro; IPR003280; K+channel 2pore.
DR InterPro; IPR001622; K+channel 2pore.
DR InterPro; IPR003976; Trek channel.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 414 AA; 45555 MW; 27F52D51DFFC66F8 CRC64;
Query Match 99.6%; Score 2082; DB 2; Length 414;
Best Local Similarity 99.5%; Pred. No. 1.5e-132;
Matches 409; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLII 60
DB 4 VAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLII 63
QY 61 GAAVFKALEQPEQISQRTTIVIQKTFIAQHACVNSTELDELIQIIVAAINAGIIPLGNS 120
DB 64 GATVFKALEQPEQISQRTTIVIQKTFIAQHACVNSTELDELIQIIVAAINAGIIPLGNS 123
QY 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIYALLGIFLPGFLAGVGQ 180
DB 124 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGKIFCIIYALLGIFLPGFLAGVGQ 183
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 240
DB 184 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAVIFKHIEGWSALD 243
QY 241 AIYFVVITLTITGFDYVAGGSDIEYDFYKPVVFWLVLGAYFAAVLSMTGDLWRVIS 300
DB 241 AIYFVVITLTITGFDYVAGGSDIEYDFYKPVVFWLVLGAYFAAVLSMTGDLWRVIS 300

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Db 244 AIYFVVITLTITGFGDYVAGGSDIEYLFYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 303
Qy 301 KKTKEEVGEFRAHAAEWNTANVTAEPKTRRRLSVEIYDKFORATSVKRKLSELAGNHNQ 360
Db 304 KKTKEEVGEFRAHAAEWNTANVTAEPKTRRRLSVEIYDKFORATSVKRKLSELAGNHNQ 363
Qy 361 ELTPCRTLNVNHLTSEREVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 411
Db 364 ELTPCRTLNVNHLTSEREVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 414

RESULT 3
Q920B6 PRELIMINARY; PRT; 426 AA.
AC Q920B6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE 2P domain potassium channel KCNK2 (Tandem pore domain potassium channel TREK-1) (Arachidonic acid sensitive tandem pore domain potassium channel)
DE Name=Kcnk2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=21219399; PubMed=11319556;
RY Bockenbauer D., Zilberberg N., Goldstein S.A.;
RT "KCNK2: reversible conversion of a hippocampal potassium leak into a voltage-dependent channel.";
RL Nat. Neurosci. 4:486-491(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=21896087; PubMed=11897838;
RY Gu W., Schlichter G., Hirsch J.R., Engels H., Karschin C., Karschin A., Derst C., Steinlein O.K., Daut J.;
RT "Expression pattern and functional characteristics of two novel splice variants of the two-pore-domain potassium channel TREK-2.";
RL J. Physiol. 539:657-668(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RY Li Z.B., Wang X.L.;
RT "Possible role of TREK-1 in temperature regulation.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
DR EMBL; AF325671; AAL01159.1; -
DR EMBL; AF385402; AAL95708.1; -
DR EMBL; AY695826; AAU06141.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
KW Ion transport; Ionic channel; Transmembrane; Transport.
SQ SEQUENCE 426 AA; 46912 MW; 646912 MW; CACDA05BBE95FDBC CRC64;

Query Match 98.6%; Score 2061; DB 2; Length 426;
Best Local Similarity 98.3%; Pred. No. 4.1e-131; Indels 0; Gaps 0;
Matches 404; Conservative 3; Mismatches 4;

Qy 1 MAAPDLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKKTSTFVLVLYLII 60
Db 16 VAAPDLDPKSAQNSKPRLSFSAKPTVLASRVESDSAINVMKKTSTFVLVLYLII 75
Qy 61 GAAVFKALPEQOEISORTTIVIKQNTIAQACVNSTELDELIOQIVTAINGIPLGNN 135

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Db 76 GATVFKALPEQOEISORTTIVIKQNTIAQACVNSTELDELIOQIVTAINGIPLGNN 135
Qy 121 SNQSHWDLGSSFFAGTVTTITGFGNISPRTEGGKIFCIIYALLGIPILFGLAGVGQD 180
Db 136 SNQSHWDLGSSFFAGTVTTITGFGNISPRTEGGKIFCIIYALLGIPILFGLAGVGQD 195
Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFPALPAVIFKHIEGHSALD 240
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFPALPAVIFKHIEGHSALD 255
Qy 241 AIYFVVITLTITGFGDYVAGGSDIEYLFYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300
Db 256 AIYFVVITLTITGFGDYVAGGSDIEYLFYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 315
Qy 301 KKTKEEVGEFRAHAAEWNTANVTAEPKTRRRLSVEIYDKFORATSVKRKLSELAGNHNQ 360
Db 316 KKTKEEVGEFRAHAAEWNTANVTAEPKTRRRLSVEIYDKFORATSVKRKLSELAGNHNQ 375
Qy 361 ELTPCRTLNVNHLTSEREVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 411
Db 376 ELTPCRTLNVNHLTSEREVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 426

RESULT 4
Q9NRT2 PRELIMINARY; PRT; 411 AA.
AC Q9NRT2;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Two-pore domain potassium channel TREK-1 (Potassium channel, subfamily K, member 2).
GN Name=TREK-1; Synonyms=KCNK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RY MEDLINE=20244931; PubMed=10784345;
RY Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C., Medhurst A.D., Murdock P., Chapman C.G.;
RT "Cloning, localisation and functional expression of the human orthologue of the TREK-1 potassium channel.";
RL Pflugers Arch. 439:714-722(2000).
RN [2]
RP SEQUENCE FROM N.A.
RY TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RY Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywicki M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RY TISSUE=PCR rescued clones;

```

RA Strausberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
 CC (TC 1.A.1.8) family.
 DR EMBL; AF171068; AAF89743.1; -.
 DR EMBL; BC069462; AAF69462.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0005267; F:potassium channel activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR GO; GO:0006813; P:ion transport; IEA.
 DR InterPro; IPR003280; K-channel_2pore.
 DR InterPro; IPR001622; K-channel_pore.
 DR PRINTS; PR01333; 2PORECHANNEL.
 DR PRINTS; PR01499; TREKCHANNEL.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 411 AA; 45494 MW; FDE40CAB21B42A1C CRC64;

Query Match 97.8%; Score 2044; DB 2; Length 411;
 Best Local Similarity 96.4%; Pred. No. 5.5e-130;
 Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPLSFSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLII 60
 DB 1 MAAPDLLDPKSAQAQNSKPLSFSTKPTVLASRVSDTTINVMKWTSTIFLVVLYLII 60
 QY 61 GAAVFKALPOEISQRTTIVIQKQTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120
 DB 61 GATVFKALQEPHEISQRTTIVIQKQTFISQHCVNSTELDELIQOIVAAINAGIPLGNT 120
 QY 121 SNOVSHWDLGSSFFPAGTIVITIGFNIISPRTEGGKIFCIIVALLGIPFGFLLAGVGQD 180
 DB 121 SNOVSHWDLGSSFFPAGTIVITIGFNIISPRTEGGKIFCIIVALLGIPFGFLLAGVGQD 180
 QY 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIGWSALD 240
 DB 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIGWSALD 240
 QY 241 AIYFVVTITLTIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVALSMIGDWLRVIS 300
 DB 241 AIYFVVTITLTIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVALSMIGDWLRVIS 300
 QY 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLKSAELAGNHQ 360
 DB 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLKSAELAGNHQ 360
 QY 361 ELTPCRRTLTSVNLHTSEREVLPLLKAEISYIYNGLTTPHCAGEDIAVIENMK 411
 DB 361 ELTPCRRTLTSVNLHTSERDVLPLLKTESIYIYNGLTTPHCAGEIAVIENIK 411

RESULT 5

Q8HY88 PRELIMINARY; PRT; 411 AA.
 AC Q8HY88;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Potassium channel subfamily K member 2.
 GN Name=Kcnk2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=adrenal cortex;
 RX MEDLINE=22370953; PubMed=1268289; DOI=10.1074/jbc.M207233200;
 RA Enyeart J.J., Xu L., Danti S., Enyeart J.A.;
 RT "An ACTH- and ATP-regulated background K+ channel in adrenocortical
 cells is TREK-1.";

RL J. Biol. Chem. 277:49186-49199(2002).
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
 CC (TC 1.A.1.8) family.
 DR EMBL; AY148474; AAN37591.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0005267; F:potassium channel activity; IEA.
 DR GO; GO:0006811; P:ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR003280; K-channel_2pore.
 DR InterPro; IPR001622; K-channel_pore.
 DR PRINTS; PR01333; 2PORECHANNEL.
 DR PRINTS; PR01499; TREKCHANNEL.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 411 AA; 45438 MW; A185EAC20A68CCDC CRC64;

Query Match 97.3%; Score 2034; DB 2; Length 411;
 Best Local Similarity 96.1%; Pred. No. 2.6e-129;
 Matches 395; Conservative 10; Mismatches 6; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPLSFSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLII 60
 DB 1 MAAPDLLDPKSAQAQNSKPLSFSTKPTVLASRVSDTTINVMKWTSTIFLVVLYLII 60
 QY 61 GAAVFKALPOEISQRTTIVIQKQTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120
 DB 61 GATVFKALQEPHEISQRTTIVIQKQTFISQHCVNSTELDELIQOIVAAINAGIPLGNT 120
 QY 121 SNOVSHWDLGSSFFPAGTIVITIGFNIISPRTEGGKIFCIIVALLGIPFGFLLAGVGQD 180
 DB 121 SNOVSHWDLGSSFFPAGTIVITIGFNIISPRTEGGKIFCIIVALLGIPFGFLLAGVGQD 180
 QY 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIGWSALD 240
 DB 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIGWSALD 240
 QY 241 AIYFVVTITLTIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVALSMIGDWLRVIS 300
 DB 241 AIYFVVTITLTIGFDYVAGGSDIEYLDYFKPVWFWILVGLAYFAAVALSMIGDWLRVIS 300
 QY 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLKSAELAGNHQ 360
 DB 301 KKTKEEVGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLKSAELAGNHQ 360
 QY 361 ELTPCRRTLTSVNLHTSEREVLPLLKAEISYIYNGLTTPHCAGEDIAVIENMK 411
 DB 361 ELTPCRRTLTSVNLHTSERDVLPLLKTESIYIYNGLTTPHCAGEIAVIENIK 411

RESULT 6

CIW2_HUMAN STANDARD; PRT; 426 AA.
 ID AC Q95069; Q9UNE3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Potassium channel subfamily K member 2 (Outward rectifying potassium
 channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore
 potassium channel TPCK1).
 GN Name=KCNK2; Synonyms=TREK, TREK1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
 RT "Inhalational anesthetics activate two-pore-domain background K+
 channels.";
 RL Nat. Neurosci. 2:422-426(1999).
 RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Price L.A., Hellings S.E., Hayaashi J.H., Pausch M.H.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Outward rectifier potassium channel.
CC -!- SUBUNIT: Homodimer (Potential).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- MISCELLANEOUS: Activated by volatile general anaesthetics such as
CC chloroform, halothane and isoflurane.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF129399; AAD47569.1; -;
CC EMBL; AF004711; AAD01203.1; -;
CC Genew; HGNC:6277; KCNK2.
CC MIM; 603219; -;
CC GO; GO:0016020; C:membrane; NAS.
CC GO; GO:0015271; F:outward rectifier potassium channel activity; NAS.
CC GO; GO:0006813; P:potassium ion transport; NAS.
CC InterPro; IPR003280; K-channel_2pore.
CC InterPro; IPR001622; K-channel_pore.
CC InterPro; IPR003976; Trek channel.
CC PRINTS; PRO1333; 2PORECHANNEL.
CC PRINTS; PRO1499; TREKCHANNEL.
CC KW Glycoprotein; Ion transport; Ionic channel; Potassium;
CC Potassium channel; Transmembrane; Transport; Voltage-gated channel.
CC FT DOMAIN 1 61 Cytoplasmic (Potential).
CC FT TRANSMEM 62 82 Potential.
CC FT DOMAIN 144 170 Pore-forming 1 (Potential).
CC FT TRANSMEM 172 192 Potential.
CC FT DOMAIN 193 223 Cytoplasmic (Potential).
CC FT TRANSMEM 224 244 Potential.
CC FT DOMAIN 253 283 Pore-forming 2 (Potential).
CC FT TRANSMEM 288 308 Potential.
CC FT DOMAIN 309 426 Cytoplasmic (Potential).
CC FT DOMAIN 378 426 Essential for chloroform and halothane
CC sensitivity (By similarity).
CC FT DOMAIN 354 426 Required for basal channel activity (By
CC similarity).
CC FT CARBOHYD 110 110 N-linked (GlcNAc...) (Potential).
CC FT CARBOHYD 134 134 N-linked (GlcNAc...) (Potential).
CC FT CONFLICT 2 16 Missing (in Ref. 2).
CC FT CONFLICT 309 311 RLV -> DWL (in Ref. 2).
CC FT CONFLICT 391 391 S -> N (in Ref. 2).
CC FT CONFLICT 411 411 A -> T (in Ref. 2).
CC SQ SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009F4E CRC64;

Query Match 96.2%; Score 2011; DB 1; Length 426;
Best Local Similarity 95.1%; Pred. No. 9, 7e-128;
Matches 391; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQN--SKPRLSFSKPTVLASRVESDSAINVMKKTSTIFLVVLYLI 60
DB 16 VAAPDLLDPKSAQN--SKPRLSFSKPTVLASRVESDTTNNVMKKTSTIFLVVLYLI 75

QY 61 GAAVFKALPQPEISQRTTIVIQKQTFIAQACVNSTELDELIQOIVAAINAGIPLGNS 120
DB 76 GATVFKALPQPEISQRTTIVIQKQTFISQHCVNSTELDELIQOIVAAINAGIPLGNT 135

QY 121 SNQVSHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIYIALLGIPFGFLLAGVGQ 180
DB 136 SNQISHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIYIALLGIPFGFLLAGVGQ 195

QY 181 LGTIFGKGIKVEDTFIKNWSQTKIRIISTIFILFGCVLVALPAVIFKHIKESALD 240

DB 196 LGTIFGKGIKVEDTFIKNWSQTKIRIISTIFILFGCVLVALPAVIFKHIKESALD 255
QY 241 AIYFVVTITLTIGFGDYVAGSDIEYLDYFKPVMFWMILVGLAYFAAVLSMIGDMLRVIS 300
DB 256 AIYFVVTITLTIGFGDYVAGSDIEYLDYFKPVMFWMILVGLAYFAAVLSMIGRLVRVIS 315
QY 301 KKTKEVGEFRAHAAEWNTAVTAEPKETRRLRSVEIYDKFORATSVKRLKSLAELAGNHQ 360
DB 316 KKTKEVGEFRAHAAEWNTAVTAEPKETRRLRSVEIYDKFORATSIKRLKSLAELAGNHQ 375
QY 361 ELTPCRRITLSVNHLSERELPPLKABSIYLNGLTPHCAGEDIIVNIENMK 411
DB 376 ELTPCRRITLSVNHLSERDVLPLPKTESIYLNGLAPHCAGEEIAVENIK 426

RESULT 7
Q6Q834 PRELIMINARY; PRT; 538 AA.
AC Q6Q834;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Potassium channel TREK-2.
GN Name=KCNK10;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Rae J.L.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
CC EMBL; AY563324; AAS66991.1; -;
CC GO; GO:0006802; C:integral to membrane; IEA.
CC GO; GO:0005216; F:ion channel activity; IEA.
CC GO; GO:0005267; P:potassium channel activity; IEA.
CC GO; GO:0006811; P:ion transport; IEA.
CC GO; GO:0006813; P:potassium ion transport; IEA.
CC InterPro; IPR003280; K-channel_2pore.
CC InterPro; IPR001622; K-channel_pore.
CC InterPro; IPR003976; Trek channel.
CC PRINTS; PRO1333; 2PORECHANNEL.
CC PRINTS; PRO1499; TREKCHANNEL.
CC KW Ion transport; Ionic channel; Transmembrane; Transport.
CC SQ SEQUENCE 538 AA; 59844 MW; 1F06C8EA0DE8CB4D CRC64;

Query Match 60.4%; Score 1261.5; DB 2; Length 538;
Best Local Similarity 65.3%; Pred. No. 4, 9e-77;
Matches 247; Conservative 56; Mismatches 64; Indels 11; Gaps 5;

QY 2 RAPDLLDPKSAQN--SKPRLSFSKPTVLASRVESDS---AINVMKKTSTIFLVVLY 56
DB 23 AAPVCPQKSAQNTNGHPAAPRLSISRATVVA-RMEGTSGQSGQSVNKMKTVAIFVWV 81

QY 57 YLIIGAAVFKALPQPEISQRTTIVIQKQTFIAQACVNSTELDELIQOIVAAINAGIIP 116
DB 82 YLVTGGLVFRALPQPEISQRTTIVIQKQTFIAQACVNSTELDELIQOIVAAINAGIIP 141

QY 117 LGNSNQVSHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIYIALLGIPFGFLLAG 176
DB 142 IGNSNNSSHWDLGSAFFAGTIVITIGVGNIAPISTEGGKIFCIYIALLGIPFGFLLAG 201

QY 177 VGDQGTITFGKIAKVEDTFIKNWSQTKIRIISTIFILFGCVLVALPAVIFKHIKES 236
DB 202 TGDQGTITFGKIAKVEDTFIKNWSQTKIRIISTIFILFGCVLVALPAVIFKHIKES 261

QY 237 SALDAIYFVVTITLTIGFGDYVAGG-SDEYLDYFKPVMFWMILVGLAYFAAVLSMIGDW 295
DB 262 TALESIIYFVVTITLTIGFGDYVAGGAGNINREWTYKPLVFWFVILVGLAYFAAVLSMIGDW 321

QY 296 LRVISKKTKEEVEFRAHAAEWNTAVTAEPKETRRLRSVEIYDKFORATSV----KRLK 351

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA The FANTOM Consortium;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Konno H., Akiyama J., Nishi K., Kitesunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishimi T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
 RA Horii F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akaiura S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
 CC EMBL: AK082153; BAC38424.1;
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005216; F:ion channel activity; IEA.
 DR GO: GO:0005267; F:potassium channel activity; IEA.
 DR GO: GO:0006811; P:ion transport; IEA.
 DR GO: GO:0006813; P:potassium ion transport; IEA.
 DR InterPro: IPR003280; K+channel_2pore.
 DR InterPro: IPR001622; K+channel_pore.
 DR InterPro: IPR003976; Trek_channel.

DR PRINTS; PRO1333; 2POREKCHANEL.
 DR PRINTS; PRO1499; TREKCHANNEL.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 535 AA; 59401 MW; 3E98E89F875C268D CRC64;
 Query Match 60.1%; Score 1256.5; DB 2; Length 535;
 Best Local Similarity 65.3%; Pred. No. 1.le-76;
 Matches 247; Conservative 55; Mismatches 65; Indels 11; Gaps 5;
 QY 2 AAPDLLDPKSA--AONSKPRLSFSSKPTVLASRVESDS---AINVMKWKTVSTIFLVVL 56
 DB 20 APPVCQPKSATNGHPVRLSISSEATVVA-RMEGASOGGLQTVMKKTVAIFVWV 78
 QY 57 YLIIGAAPKALEQPOEISQRTTIVIQOTFIAQAHCNVSTELDELIQOIVAAINAGIIP 116
 DB 79 YLVGTGLVPRALEQPPSSQKNTALEKAEFLRDHICVSPQELTETIQHALDADNAGVSP 138
 QY 117 LGNSSNOVSHWDLGSSFFPAGTVITIGFGNISPRTEGKIFCIIVALLGIPLFGLLAG 176
 DB 139 VGNSSNSHWDLGSAFFAGTVITIGYGNAPSTEGKIFCILYAIFGIPLFGLLAG 198
 QY 177 VGDQLGTIPGKIAGVEDTFIKMNVSQTKIRIISTIFILFGCVLFPALPAVIFKHIEGW 236
 DB 199 IGDQLGTIPGKSIARVEKVRKKQVSQTKIRIVISILFILAGCIVFTVPAVIFKHIEGW 258
 QY 237 SALDAIYFVITLTITIGFGDYVAGG--SDIEYLDYKPVVWVILVGLAYFAAVLSMIGDW 295
 DB 259 TALESIYFVVTLTITVGDFVAGGNAGINREWKPLVWFWILVGLAYFAAVLSMIGDW 318
 QY 296 LEVISKTKKEEYGEFRAHAETANTVAEFKTRRLSVEIYDKFORATSV-----KKLS 351
 DB 319 LEVLKTKKEEYGEIKAHAAEWKANTAEFRTRRLSVEIHDKLRQAATIRSMERRRLG 378
 QY 352 AELAGNHQELTPCRRTL 369
 DB 379 LDQRAHSLDMLSPKRSV 396
 RESULT 10
 ID_C1WA RAT STANDARD; PRT; 538 AA.
 AC Q9JFS4;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel subunit).
 DE Name=Kcnk10; Synonym=Trek2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20598907; PubMed=10747911; DOI=10.1074/jbc.M000445200;
 RA Bang H., Kim Y., Kim D.;
 RT "TREK-2, a new member of the mechanosensitive tandem-pore K+ channel family.";
 RL J. Biol. Chem. 275:17412-17419(2000).
 CC -1- FUNCTION: Outward rectifying potassium channel. Produces rapidly activating and non-inactivating outward rectifier K(+) currents. Activated by arachidonic acid and other naturally occurring unsaturated free fatty acids.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: Expressed mainly in the cerebellum, spleen, and testis.
 CC -1- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way


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FT VARSPLIC 1. 12 /FTID=VSP 006697.
FT MFLYIDFELS -> MKPEIETPRKQVNDPK (in
FT isoform C).
FT /FTID=VSP 006698.
FT CONFLICT 529 529 E -> G (in Ref. 2).
SQ SEQUENCE 538 AA; 59764 MW; 8EA615B08D147FBC CRC64;

Query Match 59.9%; Score 1251.5; DB 1; Length 538;
Best Local Similarity 64.3%; Pred. No. 2.3e-76;
Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;

QY 2 AADLLDPKSA-----AQNKPRLSPSSKPTVLASRVESDS---AINVMKKTIVSTI 50
DB 17 AADPVCQPSATNGQPPAPPTPRLSSSRATVVA-RMEGTSQGLQTVMKKTIVVAI 75
QY 51 FLVVVLYLIIGAFAVKALQPOEISQRTTIVIQKOTFFIAQHACVNSTDELIIQIIVAAI 110
DB 76 FVVVVVLYVTGLVFALQEPPESSQKNTIALEKAEFLRHVCVSPQLETLIQHALDAD 135
QY 111 NAGIPLGNSSNOVSHWDLGSSFFPAGTIVITIGFONISPRTEGKIFICIIYALLGIPLF 170
DB 136 NAGVSPIGNSSNNSSHWDLGSAFFAGTIVITIGYNIAPSTEGGKIFICILYAIIGIPLF 195
QY 171 GFLLAGVGDLGTIFGKIAGVEDTIFKWNVSQTKIRIISTIFILFGCVLFAVPAVIF 230
DB 196 GFLLAGIGDLGTIFGKISARVEKVRKQVQSQTIRKIRVISTIFILAGCIVFTIIPAVIF 255
QY 231 KHIEGWSALDAIFYFVVTITLTGFGDYVAGG-SDIEYLDYKPVVFWMLVGLAYFAAVL 289
DB 256 KYIEGWTALESIYFVVVTLTGVGDFVAGNAGINREWKPLVWFWMLVGLAYFAAVL 315
QY 290 SMIGDMLRVISKKTKEEVEGFRAHAAEWNTANTYAEFKETRRRLSVEIYDKFORATSV--- 346
DB 316 SMIGDMLRVLSKKTKEEVEGEIKAHAAEWKANTYAEFRETTRRLSVEIHDKFORAATIRSM 375
QY 347 -KRKLSAELAGNHQBLTPCRTL 369
DB 376 ERRRLGLDQRAHSLDMLSPKRSV 399

RESULT 12
Q6B014 PRELIMINARY; PRT; 543 AA.
AC Q6B014;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE Potassium channel, subfamily K, member 10, isoform 3.
GN Name=KCNK10;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled tissue;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled tissue;
RA Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075022; AAH75022.1; -.
DR EMBL; BC075021; AAH75021.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005226; F:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K:channel_pore.
DR InterPro; IPR011255; N:ir_siralpha_1/3.
DR InterPro; IPR003976; Trk_channel.
DR PRINTS; PRO1333; 2POREKCHANNEL.
DR PRINTS; PRO1499; TREKCHANNEL.
KW Ionic channel.
SQ SEQUENCE 543 AA; 60110 MW; 17DB1AFAPAB07C46 CRC64;

Query Match 59.9%; Score 1251.5; DB 2; Length 543;
Best Local Similarity 64.3%; Pred. No. 2.3e-76;
Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;

QY 2 AADLLDPKSA-----AQNKPRLSPSSKPTVLASRVESDS---AINVMKKTIVSTI 50
DB 22 AADPVCQPSATNGQPPAPPTPRLSSSRATVVA-RMEGTSQGLQTVMKKTIVVAI 80
QY 51 FLVVVLYLIIGAFAVKALQPOEISQRTTIVIQKOTFFIAQHACVNSTDELIIQIIVAAI 110
DB 81 FVVVVVLYVTGLVFALQEPPESSQKNTIALEKAEFLRHVCVSPQLETLIQHALDAD 140
QY 111 NAGIPLGNSSNOVSHWDLGSSFFPAGTIVITIGFONISPRTEGKIFICIIYALLGIPLF 170
DB 141 NAGVSPIGNSSNNSSHWDLGSAFFAGTIVITIGYNIAPSTEGGKIFICILYAIIGIPLF 200
QY 171 GFLLAGVGDLGTIFGKIAGVEDTIFKWNVSQTKIRIISTIFILFGCVLFAVPAVIF 230
DB 201 GFLLAGIGDLGTIFGKISARVEKVRKQVQSQTIRKIRVISTIFILAGCIVFTIIPAVIF 260
QY 231 KHIEGWSALDAIFYFVVTITLTGFGDYVAGG-SDIEYLDYKPVVFWMLVGLAYFAAVL 289
DB 261 KYIEGWTALESIYFVVVTLTGVGDFVAGNAGINREWKPLVWFWMLVGLAYFAAVL 320
QY 290 SMIGDMLRVISKKTKEEVEGFRAHAAEWNTANTYAEFKETRRRLSVEIYDKFORATSV--- 346
DB 321 SMIGDMLRVLSKKTKEEVEGEIKAHAAEWKANTYAEFRETTRRLSVEIHDKFORAATIRSM 380
QY 347 -KRKLSAELAGNHQBLTPCRTL 369
DB 381 ERRRLGLDQRAHSLDMLSPKRSV 404

RESULT 13
Q68EY1 PRELIMINARY; PRT; 546 AA.
ID Q68EY1
AC Q68EY1;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE LOC446298 protein (Fragment).
GN Name=LOC446298;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
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RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguercio N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC080069; AAH80069.1; -;
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR003976; Trek_channel.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
FT NON_TER 546 546
SQ SEQUENCE 546 AA; 60977 MW; AF6C7FB34AD34A06 CRC64;

Query Match 58.5%; Score 1223.5; DB 2; Length 546;
Best Local Similarity 60.6%; Pred. No. 1.8e-74;
Matches 241; Conservative 62; Mismatches 70; Indels 25; Gaps 5;

QY 18 PRLSSSKPTVLASRVESDSAI-NYMKWTSTIFLVVLYLIGAAVFKALEQPEISQ 76
DB 52 PRMSVCSRLTSTMDNTSSGHSVNMKVTIAIFVWVVVILVTGLVFRALQPFESQ 111
QY 77 RTTIVIKQTFIAQACVNSTDELIOQIVAAINAGIIPLGNSNQVSHWDLGSSFFFA 136
DB 112 KETIAEKSDFLHNPCTVQQLDALIKRAIDADNAGVNPICGNYSNHHWDLGSAFFFA 171
QY 137 GTVITITIGNTSPRTGKIKCIYVALLGIFLPGFLLAGVGDQGTIPFGKIAKVDTFF 196
DB 172 GTVITITIGNTAPSTGKIFCIYVALLGIFLPGFLLAGVGDQGTIPFGKIAKVDF 231
QY 197 IKWVYSOTKIRIISTITIFLCVLFVALPAVIFKHIGWSALDAIFYVWVLTITIGFD 256
DB 232 LKKQVSQTKIRIVISTITIFLCVLFVALPAVIFKHIGWTELESIFYVWVLTITIGFD 291
QY 257 YVAGG-SDIEYLDYFKPVVFWVWVLLVGLAYFAAVLSMIGDWLRVISKTKKEEYGEFRAHAA 315
DB 292 FVAGNNTDISYEWYKPIVFWVWVLLVGLAYFAAVLSMIGDWLRVISKTKKEEYGEIKAHAA 351
QY 316 ENTWANTAFKTRRLRSVEIYDKFORATSV----KRLKLSAELAGNHQELTPCRRTL-- 369
DB 352 ENKANVTABITRRLRSVEIHKLQRAATIRSMERRRLGLDQRAHSLDMLSPKRSVFA 411

QY 370 -----SVNHLTSEREVLPLPKAESIYLYNG 394
DB 412 ELEAGRFKASSQDSINNRPNLR----LKRAEQFTLHG 445

RESULT 14
CIW4_HUMAN
ID CIW4_HUMAN STANDARD; PRT; 393 AA.
AC Q9NYG8; O96T94;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE P05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-
DE stimulated potassium channel protein) (TRAAK) (Two pore K+ channel
DE KT4.1)
GN Name=KCNK4; Synonyms=TRAAK;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX PubMed=11042359; DOI=10.1016/S0169-328X(00)00183-2;
RA Chapman C.G., Meadows H.J., Godden R.J., Campbell D.A., Duckworth M.,
RA Kelsell R.E., Murdock P.R., Randall A.D., Rennie G.I., Gloger I.S.;
RA "Cloning, localization and functional expression of a novel human,
RA cerebellum specific, two pore domain potassium channel";
RA Brain Res. Mol. Brain Res. 82:74-83(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Frontal cortex;
RA Gray A.T.;
RT "Assignment of KCNK4 encoding the human potassium channel TRAAK to
RT chromosome 11";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=20231699; PubMed=10767409; DOI=10.1016/S0014-5793(00)01388-0;
RA Lesage F., Maingret F., Lazdunski M.;
RT "Cloning and expression of human TRAAK, a polynaturated fatty acids-
RT activated and mechano-sensitive K(+) channel";
RL FEBS Lett. 471:137-140(2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=2219385; PubMed=12191490; DOI=10.1016/S0169-328X(02)00157-2;
RA Ozaita A., Vega-Saenz de Miera E.;
RT "Cloning of two transcripts, HKT4.1a and HKT4.1b, from the human two-
RT pore K+ channel gene KCNK4. Chromosomal localization, tissue
RT distribution and functional expression";
RL Brain Res. Mol. Brain Res. 102:18-27(2002).
RN [5]
RP SPLICE ISOFORM(S) THAT ARE POTENTIAL NMD TARGET(S).
RX PubMed=14759258; DOI=10.1186/gb-2004-5-2-r8;
RA Hillman R.T., Green R.E., Brenner S.E.;
RT "An unappreciated role for RNA surveillance";
RL Genome Biol. 5:RESEARCH008.1-RESEARCH008.16(2004).
CC -!- FUNCTION: Voltage insensitive, instantaneous, outwardly rectifying
CC potassium channel. Outward rectification is reversed at high
CC external K(+) concentrations (By similarity).
CC -!- SUBUNIT: Homodimer (Potential).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=KT4.1a;
CC IsoId=Q9NYG8-1; Sequence=Displayed;
CC Name=2; Synonyms=KT4.1b;
CC IsoId=Q9NYG8-2; Sequence=VSP_006689;
CC Note=May be produced at very low levels due to a premature stop
CC codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
CC -----

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 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

CC -----
 CC EMBL: AF248242; AAK31731.1; --
 CC EMBL: AF247042; AAF64062.1; ALT_INIT.
 CC EMBL: AF259500; AAK49389.1; --
 CC EMBL: AF259501; AAK49390.1; --
 CC Genew: HGNC:6279; KCNK4.
 CC MIM: 605720; --
 CC GO: GO:005267; P:potassium channel activity; TAS.
 CC GO: GO:006813; P:potassium ion transport; TAS.
 CC InterPro: IPR003280; K+channel_2pore.
 CC InterPro: IPR001622; K+channel_pore.
 CC InterPro: IPR008074; TRAAK_CHANNEL.
 CC PRINTS: PR01333; 2POREKCHANNEL.
 CC PRINTS: PR01691; TRAAKCHANNEL.
 CC KW Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
 CC Potassium channel; Transmembrane; Transport;
 CC Voltage-gated channel.
 CC FT DOMAIN 1 3 Cytoplasmic (Potential).
 CC FT TRANSMEM 4 24 Potential.
 CC FT DOMAIN 89 113 Pore-forming 1 (Potential).
 CC FT TRANSMEM 118 138 Potential.
 CC FT DOMAIN 139 171 Cytoplasmic (Potential).
 CC FT TRANSMEM 172 192 Potential.
 CC FT DOMAIN 197 221 Pore-forming 2 (Potential).
 CC FT TRANSMEM 234 254 Potential.
 CC FT DOMAIN 255 393 Cytoplasmic (Potential).
 CC FT CARBOHYD 78 78 N-linked (GlcNAc. .) (Potential).
 CC FT CARBOHYD 82 82 N-linked (GlcNAc. .) (Potential).
 CC FT VARSPIC 1 1 M -> MTPAQEPAPPLQAGSGAGPAPGRAM (in
 CC isoform 2).
 CC FT /FTID=VSP_006689.
 CC CONFLICT 328 328 P -> L (in Ref. 2).
 CC SEQUENCE 393 AA; 42704 MW; 7F18E53A0A9AD57D CRC64;

Query Match 38.1%; Score 797; DB 1; Length 393;
 Best Local Similarity 51.1%; Pred. No. 8.1e-46;
 Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;

QY 42 MKWKTSTFLVVLVLIIGAAVFAKLEQPOEISQRTTIVIOKOTFIAOHACVNSTELDE 101
 Db 1 MRSTTLALALLVLLVSGALVFRALQEPHEQQAQREGEVREKEFRAHPCVSDQELGL 60
 QY 102 LIQQIVAAINAGIPIPLGNSNQVSH--WDLGSSFFPAGTVITITIGFNGISPRTEGGKIFC 159
 Db 61 LIKEVADALGGGADPETNSTNSHSAWDLGSAFFSGTITITIGYGNVALRTDAGRLFC 120
 QY 160 IYALLGIPFLGAGVDQIGTFKGIAKVEDTFIKWVSQTKIRIISTIFILFGC 219
 Db 121 IFYALVGIPFLGAGVDRLGSSLRHGIGIEAIFLKHVPPPELVRLVSLMFLILGC 180
 QY 220 VLFVALPAVIEKHIEGWSALDIFYVVTITITIGFGDYVAGGSDIEYDFYKPVVWFLL-279
 Db 181 LIFVLTPTTFCYMDWSKLEAIFYVITITVTFGFDYVAGADPRQSDPAYQLVWFVWL 240
 QY 280 VGLAYFAAVLSIMGDLRLVIRSKTKEVEGEFRAHAAEWANTVTA 323
 Db 241 LGLAYFASVLTITIGNLVRVSRTRAEIMGGLTAQAASWTGTVTA 284

RESULT 15

CIW4_MOUSE

ID_CIW4_MOUSE

AC_O88454;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-
 DE stimulated potassium channel protein) (TRAAK).
 GN Name=Kcnk4; Synonyms=TRAAK;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98292450; PubMed=9628867; DOI=10.1093/emboj/17.12.3297;
 RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
 RA Lazdunski M.;
 RT "A neuronal two P domain K+ channel stimulated by arachidonic acid and
 RT polyunsaturated fatty acids.";
 RL EMBO J. 17:3297-3308(1998).
 RN [2]
 RP ACTIVATION
 RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
 RT "Inhalational anesthetics activate two-pore-domain background K+
 RT channels.";
 RL Nat. Neurosci. 2:422-426(1999).
 CC -!- FUNCTION: Voltage insensitive, instantaneous, outwardly rectifying
 CC potassium channel. Outward rectification is reversed at high
 CC external K(+) concentrations.
 CC -!- SUBUNIT: Homodimer (Potential).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoID=O88454-1; Sequences=Displayed;
 CC Name=2; Synonyms=TRAAK, Truncated;
 CC IsoID=O88454-2; Sequences=VSP_006690, VSP_006691;
 CC -!- TISSUE SPECIFICITY: Expressed in brain, spinal cord and eye. Not
 CC detected in heart, skeletal muscle, liver, lungs, kidney and
 CC testis.
 CC -!- MISCELLANEOUS: Activated by arachidonic acid and other unsaturated
 CC fatty acids. Not affected by volatile general anaesthetics such as
 CC chloroform, diethyl ether, halothane and isoflurane.
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
 CC (TC 1.A.1.8) family.
 CC -----
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CC -----
 CC EMBL: AF056492; AAC40181.1; --
 CC MGD; MGI:1298234; Kcnk4.
 CC InterPro: IPR003280; K+channel_2pore.
 CC InterPro: IPR001622; K+channel_pore.
 CC InterPro: IPR008074; TRAAK_CHANNEL.
 CC PRINTS: PR01333; 2POREKCHANNEL.
 CC PRINTS: PR01691; TRAAKCHANNEL.
 CC KW Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
 CC Potassium channel; Transmembrane; Transport;
 CC Voltage-gated channel.
 CC FT DOMAIN 1 3 Cytoplasmic (Potential).
 CC FT TRANSMEM 4 24 Potential.
 CC FT DOMAIN 89 113 Pore-forming 1 (Potential).
 CC FT TRANSMEM 119 139 Potential.
 CC FT DOMAIN 140 171 Cytoplasmic (Potential).
 CC FT TRANSMEM 172 192 Potential.
 CC FT DOMAIN 198 222 Pore-forming 2 (Potential).
 CC FT TRANSMEM 235 255 Potential.
 CC FT DOMAIN 256 398 Cytoplasmic (Potential).
 CC FT CARBOHYD 81 81 N-linked (GlcNAc. .) (Potential).
 CC FT CARBOHYD 84 84 N-linked (GlcNAc. .) (Potential).
 CC FT VARSPIC 63 67 KLLVE -> KAWAI (in isoform 2).

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FT VARSPLIC 68 398 /FTid=VSP 006690.
FT Missing (in isoform 2).
FT /FTid=VSP 006691.
SQ SEQUENCE 398 AA; 43051 MW; 478A834B7B7AEC92 CRC64;

Query Match 36.9%; Score 770.5; DB 1; Length 398;
Best Local Similarity 49.8%; Pred. No. 5.1e-44;
Matches 142; Conservative 56; Mismatches 84; Indels 3; Gaps 1;

QY 42 MKWKTVSTIFLVVLYLIIGAAVFKALEQPOEISORTTIVIOKQTFIAQHACVNSTELDE 101
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MRSTTLALLALVLLYLVSGALVFOALEQPHQQAQKMDHGRDQFLRDHPCVSKSLED 60
QY 102 LIQQIVAAINAGIIP---LGNSSNQVSHWDLGSSFFFACTVTTTIGFNGNISPRTEGGKIF 158
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 FTKLIVEALGGGANPETSWTNSNHSNAWNLGSAFFSGTITTTIGYGNIVLHTDAGRLF 120
QY 159 CIIYALLGIPFGLLAGVDQLGTIFGKGIKAKVEDTFIKWNVSQTKIRIISTIIIFLFG 218
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
121 CIFYALVGIPFGMLLAGVDRGLGSSLRREGIGHIEAIFLKHVPPGLVRSLSAVLFLIG 180
QY 219 CVLFVALPAVIFKHIEGWSALDAIYFVVTITTTIGFDYVAGGSDIEYLDIFYKPVWFMI 278
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
181 CLLFVLTPTTFVSVMESWSKLEAIYFVITLTTVGFDYVPGDGTQNSPAYQPLVWFMI 240
QY 279 LVGLAYFAAVLSMIGDMLRVISKTKKEEVGEFRAHAETANVTA 323
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
241 LFGLAYFASVLTITIGNWLRAVSRRTAEMGGTLTAQAASWTGTVTA 285
```

Search completed: July 13, 2005, 08:44:31
Job time : 95.9622 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:02:40 ; Search time 21.6316 Seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-09-503-089A-4
Perfect score: 2090
Sequence: 1 MAAPLLDPKSAQNSKPL.....LNGLPHCAGSDIAVIENMK 411

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	376.5	18.0	336	2 S65566	inward rectifier p
2	351.5	16.8	330	2 JC7703	TASK-5 protein - h
3	343	16.4	329	2 T43509	probable potassium
4	329.5	15.8	336	2 T32347	outward rectifier
5	325	15.6	1001	2 T13807	potassium channel
6	289	13.8	383	2 T23182	hypothetical prote
7	286.5	13.7	334	2 T19860	hypothetical prote
8	286.5	13.7	364	2 T43361	probable potassium
9	279.5	13.4	461	2 T43394	potassium channel
10	279	13.3	393	2 T23392	hypothetical prote
11	271	13.0	392	2 T45032	hypothetical prote
12	270.5	12.9	522	2 T24265	hypothetical prote
13	269	12.9	325	2 T15584	hypothetical prote
14	266	12.7	1910	2 H88124	protein T12C9.3 [i
15	263	12.6	452	2 T21118	hypothetical prote
16	252.5	12.1	1539	2 T30037	hypothetical prote
17	247	11.8	444	2 T26229	hypothetical prote
18	245.5	11.7	513	2 T28933	hypothetical prote
19	243.5	11.7	427	2 T27681	hypothetical prote
20	237	11.3	643	2 T26616	hypothetical prote
21	236	11.3	550	2 T29557	hypothetical prote
22	231	11.1	524	2 T23907	hypothetical prote
23	229.5	11.0	484	2 T43529	probable potassium
24	229.5	11.0	519	2 T16529	hypothetical prote
25	229	11.0	528	2 T21834	hypothetical prote
26	221	10.6	443	2 T21598	hypothetical prote
27	219	10.5	1136	2 T28953	hypothetical prote
28	217	10.4	691	2 S45585	outward-rectifier
29	216.5	10.4	551	2 T16426	hypothetical prote

30	216.5	10.4	555	2 T43357	potassium channel
31	216	10.3	475	2 T27725	hypothetical prote
32	215.5	10.3	335	2 S44635	f22b7.7 protein -
33	212	10.1	307	2 H89074	protein twk-24 [im
34	212	10.1	485	2 T24201	hypothetical prote
35	209.5	10.0	586	2 T21683	hypothetical prote
36	206.5	9.9	660	2 T21551	hypothetical prote
37	205	9.8	700	2 T27364	hypothetical prote
38	204.5	9.8	523	2 T23373	hypothetical prote
39	204.5	9.8	544	2 T43364	potassium channel
40	204.5	9.8	576	2 T43363	potassium channel
41	202.5	9.7	769	2 T27550	hypothetical prote
42	199.5	9.5	539	2 T23700	hypothetical prote
43	196.5	9.4	681	2 T19429	hypothetical prote
44	194.5	9.3	569	2 T43531	probable potassium
45	192.5	9.2	381	2 T43393	potassium channel

ALIGNMENTS

RESULT 1

S65566
inward rectifier potassium channel TWIK-1 - human
C:Species: Homo sapiens (man)
C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S65566
R:Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin, EMO J. 15, 1004-1011, 1996
A:Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel A:Reference number: S65566; MUID:96183184; PMID:8605869
A:Accession: S65566
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <LES>
A:Cross-references: UNIPROT:O00180; EMBL:U33632; NID:g1086490; PIDN:AAB01688.1; PID:g10

Query Match 18.0%; Score 376.5; DB 2; Length 336;
Best Local Similarity 32.5%; Pred. No. 6.3e-23;
Matches 90; Conservative 62; Mismatches 108; Indels 17; Gaps 9;

QY	51	FLVV--VLIIITAAVFAKLEQOEISQRTTIVIQKTFIAQHACVNSTELDLIIQIIVA	108
DB	25	FLVGLYLLVFGVAVFSSVELPDLRLQELKLRFRLEBHECLSEQOQLGRVLE	84
QY	109	AINAGIIPILGSSNOVSHWDLGSSPFFACTVITIGFNGISPRTEGGKIFCIYALLGIP	168
DB	85	ASNYGVSVLSNASGN-WNWDFTSALFFASTVLTGTGHTVPLSDGGAFCIIYSVIGIP	143
QY	169	LFGFLLAGVGDQLGTIFGKGIARVEDTFIKMNVSTQKIRIISTII--FILFGCVLPVALP	226
DB	144	FTLLFLTAVVQRITVHVTR--RPVLVPHIRMGFSKQVVAIHAVLLGFVTVSCFFFI--P	199
QY	227	AVIFKHIE-GWSALDAIFVWITLTITIGFDYVAG-GSDIEYLDFFKPVVWFILGLAY	284
DB	200	AAVFSVLEDDWNFLSEFYFCFISLTIGLDYVPGEYGNQKPRELYKIGITCYLLGLIA	259
QY	285	FAAVLSMIGDMLRVISK-----KTKEEVGEFRAHAAE	316
DB	260	MLVLETFCF-LHELKKFRKPFYVKDDEQVHIIE	295

RESULT 2

JC7703
TASK-5 protein - human
C:Species: Homo sapiens (man)
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: JC7703
R:Kim, D.; Gnatenko, C. Biochem. Biophys. Res. Commun. 284, 923-930, 2001
A:Title: TASK-5, a new member of the tandem-pore K+ channel family.
A:Reference number: JC7703; MUID:21303050; PMID:11409881
A:Accession: JC7703


```
Query Match      15.6%; Score 325; DB 2; Length 1001;
Best Local Similarity 28.8%; Pred. No. 3.5e-18;
Matches 90; Conservative 62; Mismatches 125; Indels 36; Gaps 10;

QY 50 IFLVVVLYLIIGAAVFKALEQOE-----ISQRTTIVIQKTFIAQHACVNSTELDELIOQ 105
DB 9 LLIFYSYLMFAGAAIYYHHGEKEKISRAEQAKIAINEYLLLELGDKNKTTTQDEILQR 68

QY 106 IVAANAGIIPLGNSNQVSHDLGSSFFPAGTIVTTIGFNGISPRTEGKIFCIYALL 165
DB 69 ISDYCDKPVTLPTTDDTYTTFYHAFPAFTVSTVGYNISPTTFAGRMIMATYSVI 128

QY 166 GIPFGFLLAGVDQDQITFGKIAKVEDTFIKMNV-----QTKIRIISTIIIFLP-G 218
DB 129 GIPVNGILFAG-----LGEYFGRTFEAIRYRYKXKXMTDMHVPVPPGLITTTWIALIPG 184

QY 219 CVLFVALPAVIFKHIEGNSALDAIYFVVTITLTIGFGDYVA-----CGSDIEYLD 268
DB 185 IALFLLPSWVFTYFENWPYSISLYSYVTTTTIGFDYVPTFGANQPKFEGGVVVYQI 244

QY 269 FYKPVVWFILVGLAYFAAVALSMIGDMLRVISKK----TKEEVGFRAHAAEWTANVTAE 324
DB 245 FV--IWWP--IFSLGYLWIMTFITRGLQ--SKLAYLEQQLSSNLKATQNRWISGVTKD 298

QY 325 FKETRRLSVEIY 337
DB 299 VGYLRLMLN-ELY 310

RESULT 6
T23182
hypothetical protein K01D12.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23182
R:Dobson, R.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19703
A:Accession: T23182
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-383 <WIL>
A:Cross-references: UNIPROT:Q21094; EMBL:Z75543; PIDN:CAA99871.1; GSPDB:GN00023; CESP:K0
A:Experimental source: clone K01D12
C:Genetics:
A:Gene: CESP:K01D12.4
A:Map position: 5
A:Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

Query Match      13.8%; Score 289; DB 2; Length 383;
Best Local Similarity 24.2%; Pred. No. 9.2e-16;
Matches 88; Conservative 80; Mismatches 122; Indels 74; Gaps 14;

QY 15 NSKPLRSFSKPTVLASRVESDSAINVMKWTSTIFLVVLYLIIGAAVFKALEQOE 74
DB 19 NTLPSITRAKVGCFARLRIYEENARFV-----ICILIVYLAFGAILFHWLEWENEV 71

QY 75 SORTII---VIQKTFIAQHACVNSTELDELIOQIVAAINAGIIPLGNSNQVSHDLG 131
DB 72 DERIAIDNRADYQKYCKHKLNECDPEEMVRFISDGTATSGLL---NSRSRFDH--LG- 125

QY 132 SFFPAGTIVTTIGFNGISPRTEGKIFCIYALLG-----IPLFGFLLAGVDQDQITFGK 187
DB 126 SLFFSATVISTIGFTSTPTHTLGRFTIIVYGVGCTCCVLFNFLL-----RELVTGMSY 181

QY 188 GIAKVEDTFIKNVSTQKIRIISTII-----FILFG-C 219
DB 182 ILRSLRERKIRYRLKESGNKPTVLLNNEDEFNESSSCGGHMDNRWPSYVKVFILFSMC 241

QY 220 VLFVALPAVIFKHIEGNSALDAIYFVVTITLTIGFDYVAGSDIEYL--DYPKPVVWF 277
DB 242 LVLITASAGIYSVENWNYIDSLYFCIFSFATIGFDYVSNQODVTRMSPDLYRFVNFCL 301
```

```
QY 278 ILVGLAYF-----AAVLSMIGDMLRVISKTKKEEVEGFRAHAAEWTANVTAEFKETR 330
DB 302 LTLGACFFVCLSNVSSIVVRQLLNMW---IKQMDVKV-EDRSFLC-----FKKKRR 348

QY 331 RLSV 334
DB 349 YNGL 352

RESULT 7
T19860
hypothetical protein C40C9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19860
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19860
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-334 <WIL>
A:Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.1
A:Map position: X
A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match      13.7%; Score 286.5; DB 2; Length 334;
Best Local Similarity 28.7%; Pred. No. 1.3e-15;
Matches 90; Conservative 58; Mismatches 113; Indels 53; Gaps 12;

QY 50 IFLVVVLYLIIGAAVFKALEQOEISQRTTIV---IQKTFIAQHACVNSTELDELIOQI 106
DB 14 LILSTFTYLLFGAMVFDKLE-----SEKDTWVRDIERITDLKKK-YNFSERD---LHL 64

QY 107 VAAINAGIIPLGNSNQVSH-WDLGSSFFPAGTIVTTIGFNGISPRTEGKIFCIYALL 165
DB 65 FEAIKISIP-----QQAGYQWQFAGAFVATVITTVGYGHSAPSTNAGKLFMIFALF 119

QY 166 GIPFGFLLAGVDQDQITFGKIAKVEDTFIK-----WNVSTQKIRIIS-TIIFILFG 218
DB 120 GYPMGLIMFQIGERVNTFIAYSLKFRDSLHQOQFTCLQEVTPTHLLMVSLTIGPMV-- 177

QY 219 CVLFVALPAVIFKHIEGNSALDAIYFVVTITLTIGFGDYV--AGGSDIEYLDYFKPVWF 276
DB 178 ----IVSGTYMHTTEKWSIFDAYIFCMITFTIGFDLVPLOQVNALQDQLYVPATIM 233

QY 277 WILVGLAYFAAVALSMIGDMLRVISKTKKEEVEGFRAHAAEWTANVTAEFKETRRLSVEI 336
DB 234 FILIGLAVFSACVNLL-----VLGFMASNADEVTA-----AQREPPSAIV 273

QY 337 YDKFORATSVKRL 350
DB 274 LERFTRNSLVDSQI 287

RESULT 8
T43361
probable potassium channel chain n2p20 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43361
R:Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in C. elegans.
A:Reference number: Z22450
A:Accession: T43361
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-364 <WAN>
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RESULT 11
T45032
hypothetical protein Y39B6.f [imported] - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45032
R:Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berkis, M.; Bonfield, J.; Fraser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders Nature 368, 32-38, 1994
A:Authors: Showkneen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammock, L.; Wilkinson-Sproat, J.; Wohldman, P.
A:Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of *C. elegans*

A:Reference number: S43531; MUID:94150718; PMID:7906398
A:Accession: T45032
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-392 <WIL>
A:Cross-references: EMBL:AL132896; NID:G6434440; PIDN:CAB60911.1; PID:G6434446
A:Experimental source: clone Y3986B
C:Genetics:
A:Map position: 3
A:Introns: 47/2; 82/2; 106/3; 151/1; 220/1; 260/3; 370/3
A>Note: Y3986B.f

Query Match 13.0%; Score 271; DB 2; Length 392;
Best Local Similarity 25.8%; Pred. No. 2.7e-14;
Matches 82; Conservative 65; Mismatches 109; Indels 62; Gaps 12;

QY 7 LDPKSAQNS-----KPLRSFSKPTVLAS---RVESDSAINVMKWTSTIFLVVLY 57
DB 64 LEPRTSAHQSLLYPVEFKWAIAKEMSFYSDQKPKFHFHFFSLKISKLPKAKRY----- 117

QY 58 LIIGAAVFKALEQOEISQRTTIVIQOTFIAQ--HACVNSTELDELIQOI--VAAINAGI 114
DB 118 -----FSRIEYPLEKIEREAYLDYQNMQRDLIQLDIDSEIDKPLNIREAALNG-- 168

QY 115 IPLGNSNQSHDLGSSFFAGTIVTTTIGFNGISPRTEGGKIFCIYIALLGPIPLFGFL 174
DB 169 IWNDRNLTSDPNWTFCQAFFFAGTILSTVGYGRVSPRTBYGKLTILYCVIGIPLTALL 228

QY 175 AGV-----GDQLTIFGKIAKVEDFFIKWNVSTQTKIRIISTIFILFGC 219
DB 229 SAIVARMRPSHKRLGMLNORLGHF-----TVNHIQLIHGVV--VFASL 271

QY 220 VLVF-ALPAVIFKHIE-GWSALDAIYFVVTITTTIGFGDYVAGGS--DIYLDYFKPVWF 276
DB 272 LLFVFAIPAWVFSSITDSYLDAFYCYFSLTTLGLDFEPGDDNQSPRGYKIGATV 331

QY 277 WILVGLAYFAAVLSMTGD 294
DB 332 YLMGGGLCCMWLFLATLYD 349

RESULT 12
T24265
hypothetical protein T01B4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24265
R:Wilkinson, J.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19866
A:Accession: T24265
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-522 <WIL>
A:Cross-references: UNIPROT:Q22042; EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN000028; CESP:T01B4
A:Experimental source: clone T01B4
C:Genetics:
A:Gene: CESP.T01B4.1
A:Map position: X
A:Introns: 95/3; 142/1; 224/3; 290/1; 458/1

Query Match 12.9%; Score 270.5; DB 2; Length 522;
Best Local Similarity 23.7%; Pred. No. 4.2e-14;
Matches 102; Conservative 64; Mismatches 136; Indels 129; Gaps 15;

QY 50 IFLVVLYLIIGAAVFKALEQOE-----ISQRTTIVIQOTFIAQHACVNSTE 98
DB 41 LILILGYACLGGMFQALEYDQOLEAEKRVLSSESLAVNLEHLKOMNCCQSNE 100

QY 99 LDELIQOIVAINAGIIPIGNSS-NQVSHDLGSSFFAGTIVTTTIGFNGISPRTEGGKI 157
DB 101 -----KRCLELITKTIQSRDEERGEGWRWDFWNSVFFSATIPTTTIGYGNLACKNLGRI 155

QY 158 FCIIVALLGPIPLFGFLLAGVGD-----QLGTIFGKG 188
DB 156 ATIIYIGMIGLMLFVLKNFGLCKVAKKIOFNVOQCLKCFGRKQKASSLASITSE 215

QY 189 IAKV-----EDTF--IKNVSTQTKIRIISTIFILFGCVLFAVPAVIFKHIEGWS 237
DB 216 MLEVFPEVPEDDKEDTTFQLRWG-----LLVIVLFFVLCSFVVSFWENWD 260

QY 238 ALDAIYFVVTITTTIGFGDYVAGGSIDIEYLDYFKPVVWFIL--VGLAYFAAVLSMIGD- 294
DB 261 FLTAFFVFPVSLSTIGFGDIVP-----DHPRTACALFVLVFIGLAFAMVYAILQER 312

QY 295 -----W-LRVISKTKBEVGEFRAHAAEWANVT----- 322
DB 313 VENQYMWALELIDQYQEKLKQDMYDEDEKADKNDMHFSKKEPVGRGPRILLQDLLRGPD 372

QY 323 ASFKETRRRLS-----VEIYDKFORATSVKREKLSAEL-----AGNHNOELTPCRRTLS 370
DB 373 LKISGRSSSSDASSVITEASDETRHFKVGRAILAEAPDERASNHGTQLNSC--TVS 430

QY 371 VNHLTSEREVL 381
DB 431 NEHDSQOIEAI 441

RESULT 13
T15584
hypothetical protein C24A3.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15584
R:Favell, T.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C24A3.
A:Reference number: Z18373
A:Accession: T15584
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-325 <FAV>
A:Cross-references: EMBL:U40424; NID:G1065542; PID:G1065543; PIDN:AAA81455.1; CESP:C24A3
A:Gene: CESP:C24A3.6
A:Introns: 21/1; 63/3; 131/1; 193/3; 206/3

Query Match 12.9%; Score 269; DB 2; Length 325;
Best Local Similarity 25.4%; Pred. No. 3.2e-14;
Matches 87; Conservative 53; Mismatches 87; Indels 116; Gaps 11;

QY 46 TVSTIF-----LVVLYLIIGAAVFKALEQOEISQRTTIVIQOTFIAQHACVN 95
DB 10 TILTTTQKTFKGLLPLIILVAVTLGAWTFWMIEGENE---REMLTEQOK----- 56

QY 96 STELDELIOQIVAAIN-----AGIIPLGNSNOVS 125
DB 57 ---ERDELIRRTYKINQIKQRMLMTABEENYNTAKVLTTFQETLGIIPA--DMDKOI 112

QY 126 HMDLGSSFFAGTIVTTTIGFNGISPRTEGGKIFCIYIALLGPIPLFGFLAGVGDQLGTIF 185
DB 113 HWTFLGSIYCMYVTVTTIGYGNIVPCTGWRGRTATILYAFIGIPLTVLSLY----CLGSLF 168

QY 186 GKGIKAVEDTFIKWNVSTQTKIRIIS----- 210
DB 169 AKGCKMLWRFFLK-----STRVSKDLSNKLISEAADNIEEGTATTPTSAEKTENNDDDL 222

QY 211 ---TIIFILFGCVLFAVPAVIFKHIEGWSALDAIYFVVTITTTIGFGDYVAGGSIDIEYL 267
DB 223 LSFPSGLLITIVIVIFCAVLFTLEEDWDFGTSYFTLISFTTIGFGDILP--SDYDFM 280

QY 268 DFYKPVWFWILVGLAYFAAVLSMIGDMLRVIS-----KKTKE 305
DB 281 ----FIVGVLLIIGLSLSTVMTLIQQOIEALASVRRRRKKKK 319

[illegible]

QY 68 LEOPQE-----ISOKTIVIVQKQFIAGHACVNSFIELD-----LII-----Q 104
Db 222 LESPNEDLRKETGRKTTAEMRSLIYK---INNEKEVWKEDIEKELMLYSEKLYKAFKE 278
QY 105 QIVAAINAGIIPL-----GNSNQVSH-----WDLGSSFFFAK 137
Db 279 QYVRYSDVRIIGEGRSYEADETGDSERKRRHGNKRGDSKQWTTSSALFFAA 338
QY 138 TVTITIGFNGISPRTEGGKIFCIYIYALGLPLFGFLLAGVGDQIG--TIF-----GKGIA 190
Db 339 TWTATIGYGNIVPTPLGRILACVLFALFGAPIAITITIGDLGKFLSECTIWLKYKMRKGS 398
QY 191 KVEDTEIKW-----NVSTKIRIISTIIIFILFGCV 220
Db 399 RLDSAWKFRGLEDSISDDLESASKNQDSSILDMWDDEIDKSEVPVLMVFTII-----L 452
QY 221 LFVALPAVIFKHIEGWSALDAIYVVTITLTITIGFQDVVAGGSDIEYLDYFKYVWFVILV 280
Db 453 LYIAFGGILFSLIEDWSYMDAFYYSFISLTITIGFGDIVPENHD-----YIAIMLYLGV 506
QY 281 GLAYFAAVLNMIG-----DWLRVISKTK-----EVGGEFRAH 313
Db 507 GLSVTTWCIDLAGIQYQKIHYGFRKQGTDLLOYLKKRMLEERLANGQGEHILRYVH 566
QY 314 AAETANTVTAFFKETRRRLSVEIYDK 339
Db 567 AVE-----KFEREQEQLOQKMBEE 585

RESULT 15
T21118
hypothetical protein F1908.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21118
R:Swinsburne, J.; Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19377
A:Accession: T21118
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-452 <WIL>
A:Cross-references: UNIPROT:Q93531; EMBL:Z78541; PIDN:CAB01740.1; GSPOB:GN00028; CESP:FT

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:40:02 ; Search time 90.2442 Seconds
(without alignments)
1759.475 Million cell updates/sec

Title: US-09-503-089A-4
Perfect score: 2090
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 386332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2084	99.7	411	9 US-09-828-746-6	Sequence 6, Appl
2	2044	97.8	411	9 US-09-828-746-2	Sequence 2, Appl
3	2044	97.8	411	14 US-10-121-746-83	Sequence 83, Appl
4	2044	97.8	411	16 US-10-745-210-2	Sequence 2, Appl
5	2044	97.8	411	16 US-10-349-528-31	Sequence 31, Appl
6	2044	97.8	411	17 US-10-976-644-83	Sequence 83, Appl
7	2044	97.8	411	17 US-10-976-647-83	Sequence 83, Appl
8	2041	97.7	411	11 US-09-892-360-18	Sequence 18, Appl
9	2038	97.5	422	16 US-10-349-528-20	Sequence 20, Appl
10	2011	96.2	426	8 US-08-816-011-45	Sequence 45, Appl
11	2011	96.2	426	17 US-10-870-492-45	Sequence 45, Appl

12	2007	96.0	426	17	US-10-870-492-57	Sequence 57, Appl
13	2006	96.0	426	17	US-10-870-492-58	Sequence 58, Appl
14	2003	95.8	426	17	US-10-870-492-60	Sequence 60, Appl
15	2002	95.8	426	17	US-10-870-492-59	Sequence 59, Appl
16	1855	88.8	370	9	US-09-939-484-8	Sequence 8, Appl
17	1855	88.8	370	9	US-09-939-483-8	Sequence 8, Appl
18	1256.5	60.1	538	9	US-09-729-920-5	Sequence 5, Appl
19	1256.5	60.1	538	16	US-10-887-932-5	Sequence 5, Appl
20	1251.5	59.9	526	9	US-09-729-920-4	Sequence 4, Appl
21	1251.5	59.9	526	16	US-10-887-932-4	Sequence 4, Appl
22	1251.5	59.9	538	11	US-09-892-360-2	Sequence 2, Appl
23	1251.5	59.9	538	18	US-10-923-035-46	Sequence 46, Appl
24	1251.5	59.9	543	9	US-09-729-920-2	Sequence 2, Appl
25	1251.5	59.9	543	10	US-09-852-386-73	Sequence 73, Appl
26	1251.5	59.9	543	14	US-10-332-175-2	Sequence 2, Appl
27	1251.5	59.9	543	15	US-10-262-511-106	Sequence 106, Appl
28	1251.5	59.9	543	16	US-10-887-932-2	Sequence 2, Appl
29	1224	58.6	724	15	US-10-332-447-10	Sequence 10, Appl
30	797	38.1	392	9	US-09-747-835A-55	Sequence 55, Appl
31	797	38.1	392	15	US-10-312-312-55	Sequence 55, Appl
32	797	38.1	393	14	US-10-243-035-2	Sequence 2, Appl
33	797	38.1	419	9	US-09-828-035-2	Sequence 2, Appl
34	797	38.1	419	14	US-10-345-680-44	Sequence 44, Appl
35	797	38.1	419	14	US-10-146-733-29	Sequence 29, Appl
36	797	38.1	419	15	US-10-352-684A-8	Sequence 8, Appl
37	797	38.1	419	15	US-10-391-399-19	Sequence 19, Appl
38	797	38.1	419	16	US-10-768-158-12	Sequence 12, Appl
39	797	38.1	481	18	US-10-852-707-65	Sequence 65, Appl
40	797	38.1	822	18	US-10-852-707-64	Sequence 64, Appl
41	797	38.1	1314	9	US-09-747-835A-29	Sequence 29, Appl
42	797	38.1	1314	15	US-10-312-312-29	Sequence 29, Appl
43	770.5	36.9	398	11	US-09-892-360-19	Sequence 19, Appl
44	726	34.7	924	18	US-10-852-707-66	Sequence 66, Appl
45	726	34.7	1125	18	US-10-852-707-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-828-746-6
; Sequence 6, Application US/09828746
; Patent No. US20020028485A1
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-6

Query Match	99.7%	Score 2084;	DB 9;	Length 411;
Best Local Similarity	99.8%;	Pred. No. 5.5e-189;		
Matches 410;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKKTSTFLVVVLYLII	60	
Db	1	MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKKTSTFLVVVLYLII	60	
Qy	61	GAAPFKALEQOPEISQRTTIVIQKTFIAQACVNSTELDELIIQIVAAINAGIPLGNS	120	

Db 61 GAAVFKALEQPOEISQRTTIVIKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120
QY 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
Db 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPFAVIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPFAVIFKHIEGWSALD 240
QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300
Db 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSIAELAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSIAELAGNHQ 360
QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411
Db 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411

RESULT 2

US-09-828-746-2
; Sequence 2, Application US/09828746
; Publication No. US20020028485A1
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-2

Query Match 97.8%; Score 2044; DB 9; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-185;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTFIVLVVLYLII 60
Db 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTFIVLVVLYLII 60
QY 61 GAAVFKALEQPOEISQRTTIVIKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120
Db 61 GATVFKALEQPOHEISQRTTIVIKQTFISQHSVCNSTELDELIQIIVAAINAGIIPLGNT 120
QY 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
Db 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPFAVIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPFAVIFKHIEGWSALD 240
QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300
Db 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSIAELAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSIAELAGNHQ 360
QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411
Db 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411

QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSIAELAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSIAELAGNHQ 360
QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411
Db 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENIK 411

RESULT 3

US-10-121-746-83
; Sequence 83, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-121-746-83

Query Match 97.8%; Score 2044; DB 14; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-185;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTFIVLVVLYLII 60
Db 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTFIVLVVLYLII 60
QY 61 GAAVFKALEQPOEISQRTTIVIKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120
Db 61 GATVFKALEQPOHEISQRTTIVIKQTFISQHSVCNSTELDELIQIIVAAINAGIIPLGNT 120
QY 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
Db 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPILFGLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPFAVIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPFAVIFKHIEGWSALD 240
QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300
Db 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSIAELAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSVKRLSIAELAGNHQ 360
QY 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENMK 411
Db 361 ELTPCRRTLNVNHLTSEREVLPLPKAESIYINGLTPHCAGEDIAVIENIK 411

RESULT 4

```
US-10-745-210-2
; Sequence 2, Application US/10745210
; Publication No. US20040143855A1
; GENERAL INFORMATION:
; APPLICANT: TONONI, Giulio
; APPLICANT: CIRELLI, Chiara
; TITLE OF INVENTION: ION CHANNELS AS TARGETS FOR SLEEP-RELATED DRUGS
; FILE REFERENCE: 054030-0044
; CURRENT APPLICATION NUMBER: US/10/745,210
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/436,201
; PRIOR FILING DATE: 2001-12-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-745-210-2

Query Match          97.8%; Score 2044; DB 16; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-185;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
QY 61 GAAVFKALQPOEISORTTIVIQKOTFIAQHACVNSTELDELQIQIIVAAINAGIIPLGNS 120
DB 61 GATVFKALQPOEISORTTIVIQKOTFISQHCVCNSTELDELQIQIIVAAINAGIIPLGNT 120
QY 121 SNQVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVGQD 180
DB 121 SNQISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTPIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
DB 181 LGTIFGKGIKVEDTPIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVVWFVWILVGLAYFAAVLSMIGDMLRVIS 300
DB 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVVWFVWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRKLAEAGNHNQ 360
DB 301 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRKLAEAGNHNQ 360
QY 361 ELTPCRTLTVSNHLSERVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 411
DB 361 ELTPCRTLTVSNHLSERDVLPLPKTESIYLNGLTPHCAGEBIAVIENIK 411

RESULT 5
US-10-349-528-31
; Sequence 31, Application US/10349528
; Publication No. US20040253668A1
; GENERAL INFORMATION:
; APPLICANT: RAMANATHAN, Chandra
; APPLICANT: GOPAL, Shuba
; APPLICANT: MINTIER, Gabe
; APPLICANT: FEDER, John
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
; FILE REFERENCE: D0210
; CURRENT APPLICATION NUMBER: US/10/349,528
; CURRENT FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
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US-10-349-528-31

Query Match          97.8%; Score 2044; DB 16; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-185;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
QY 61 GAAVFKALQPOEISORTTIVIQKOTFIAQHACVNSTELDELQIQIIVAAINAGIIPLGNS 120
DB 61 GATVFKALQPOEISORTTIVIQKOTFISQHCVCNSTELDELQIQIIVAAINAGIIPLGNT 120
QY 121 SNQVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVGQD 180
DB 121 SNQISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTPIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
DB 181 LGTIFGKGIKVEDTPIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVVWFVWILVGLAYFAAVLSMIGDMLRVIS 300
DB 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVVWFVWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRKLAEAGNHNQ 360
DB 301 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRKLAEAGNHNQ 360
QY 361 ELTPCRTLTVSNHLSERVLPLPKAESIYLNGLTPHCAGEDIAVIENMK 411
DB 361 ELTPCRTLTVSNHLSERDVLPLPKTESIYLNGLTPHCAGEBIAVIENIK 411

RESULT 6
US-10-976-644-83
; Sequence 83, Application US/10976644
; Publication No. US20050112662A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, Andrew P.
; APPLICANT: CURRAN, Mark Edward
; APPLICANT: HU, Ping
; APPLICANT: RUTTER, Marc
; APPLICANT: WANG, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/976,644
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US/09/336,643
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-976-644-83

Query Match          97.8%; Score 2044; DB 17; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-185;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
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QY 61 GAAVFKALEQPOEISORTTIVIQKTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120
DB 61 GATVFKALEQPOEISORTTIVIQKTFISQHSVNSTELDELIQOIVAAINAGIPLGNT 120
QY 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLAGVGQD 180
DB 121 SNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
QY 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAIVLSMIGDWLRVIS 300
DB 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAIVLSMIGDWLRVIS 300
QY 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
DB 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
QY 361 ELTPCRRTLSVNHLTSEBVLPLLKABSIYVNGLTTPHCAGEDIAVIENMK 411
DB 361 ELTPCRRTLSVNHLTSEBVLPLLKABSIYVNGLTTPHCAGEDIAVIENMK 411

RESULT 7

US-10-976-647-83
; Sequence 83, Application US/10976647
; Publication No. US20050112663A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/976,647
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/336,643
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-976-647-83

Query Match 97.8%; Score 2044; DB 17; Length 411;
Best Local Similarity 96.4%; Pred. No. 3.5e-185;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTINVMKWTSTIFLVVLYLII 60
QY 61 GAAVFKALEQPOEISORTTIVIQKTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120
DB 61 GATVFKALEQPOEISORTTIVIQKTFISQHSVNSTELDELIQOIVAAINAGIPLGNT 120
QY 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLAGVGQD 180
DB 121 SNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240

DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
QY 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAIVLSMIGDWLRVIS 300
DB 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAIVLSMIGDWLRVIS 300
QY 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
DB 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
QY 361 ELTPCRRTLSVNHLTSEBVLPLLKABSIYVNGLTTPHCAGEDIAVIENMK 411
DB 361 ELTPCRRTLSVNHLTSEBVLPLLKABSIYVNGLTTPHCAGEDIAVIENMK 411

RESULT 8

US-09-892-360-18
; Sequence 18, Application US/09892360
; Publication No. US20040101833A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: ROMEO, GEORGES
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
; TITLE OF INVENTION: RILUZOLE
; FILE REFERENCE: 1256-R-00
; CURRENT APPLICATION NUMBER: US/09/892,360
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 60/214,559
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-892-360-18

Query Match 97.7%; Score 2041; DB 11; Length 411;
Best Local Similarity 96.1%; Pred. No. 6.7e-185;
Matches 395; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAAPDLLDPKSAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTINVMKWTSTIFLVVLYLII 60
QY 61 GAAVFKALEQPOEISORTTIVIQKTFIAQHACVNSTELDELIQOIVAAINAGIPLGNS 120
DB 61 GATVFKALEQPOEISORTTIVIQKTFISQHSVNSTELDELIQOIVAAINAGIPLGNT 120
QY 121 SNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLAGVGQD 180
DB 121 SNQISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEGWSALD 240
QY 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAIVLSMIGDWLRVIS 300
DB 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVWFILVGLAYFAAIVLSMIGDWLRVIS 300
QY 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
DB 301 KKTKEEVEGFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
QY 361 ELTPCRRTLSVNHLTSEBVLPLLKABSIYVNGLTTPHCAGEDIAVIENMK 411
DB 361 ELTPCRRTLSVNHLTSEBVLPLLKABSIYVNGLTTPHCAGEDIAVIENMK 411

RESULT 9


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; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-45

Query Match          96.2%; Score 2011; DB 17; Length 426;
Best Local Similarity 95.1%; Pred. No. 5e-182;
Matches 391; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTFIPLVVVLYLII 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTFIPLVVVLYLII 75
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GAAVFKALEQPOEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 GATVFKALEQPEHISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 135
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 SNQSHWDLGSSFFPAGTIVITIGFNIQSPRTGGKIFCIIYALLGIPFLGFLAGVGDQ 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 136 SNQSHWDLGSSFFPAGTIVITIGFNIQSPRTGGKIFCIIYALLGIPFLGFLAGVGDQ 195
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFCVLFVALPAVIFKHIEGWSALD 240
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFCVLFVALPAVIFKHIEGWSALD 255
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVMFWILVGLAYFAAIVLSMIGDLVRVIS 300
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 256 TIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVMFWILVGLAYFAAIVLSMIGDLVRVIS 315
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 301 KKTKEEVGEFRAHAAEWNTANVTAFKETRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 316 KKTKEEVGEFRAHAAEWNTANVTAFKETRRLSVEIYDKFORATSVKRLSAELAGNHQ 375
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 361 ELTPCRRTLSVNHLTSREVLPLLKASIIYLNGLTPHCAGEDIAVIENMK 411
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 376 ELTPCRRTLSVNHLTSREVDLPPLKTESIYLNGLAPHAGEEIAVIENIK 426
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 13
US-10-870-492-58
; Sequence 58, Application US/10870492
; Publication No. US20050032165A1
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/816,011
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-58

Query Match          96.0%; Score 2006; DB 17; Length 426;
Best Local Similarity 94.9%; Pred. No. 1.5e-181;
Matches 390; Conservative 14; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSSKPTVLASRVESDSAINVMKWTSTFIPLVVVLYLII 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTFIPLVVVLYLII 75
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 GAAVFKALEQPOEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 GATVFKALEQPEHISQRTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 135
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 SNQSHWDLGSSFFPAGTIVITIGFNIQSPRTGGKIFCIIYALLGIPFLGFLAGVGDQ 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 136 SNQSHWDLGSSFFPAGTIVITIGFNIQSPRTGGKIFCIIYALLGIPFLGFLAGVGDQ 195
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFCVLFVALPAVIFKHIEGWSALD 240
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFCVLFVALPAVIFKHIEGWSALD 255
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 AIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVMFWILVGLAYFAAIVLSMIGDLVRVIS 300
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 256 TIYFVWITLTITIGFDYVAGGSDIEYLDYFKPVVMFWILVGLAYFAAIVLSMIGDLVRVIS 315
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 301 KKTKEEVGEFRAHAAEWNTANVTAFKETRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 316 KKTKEEVGEFRAHAAEWNTANVTAFKETRRLSVEIYDKFORATSVKRLSAELAGNHQ 375
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 361 ELTPCRRTLSVNHLTSREVLPLLKASIIYLNGLTPHCAGEDIAVIENMK 411
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 376 ELTPCRRTLSVNHLTSREVDLPPLKTESIYLNGLAPHAGEEIAVIENIK 426
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RESULT 12
US-10-870-492-57
; Sequence 57, Application US/10870492
; Publication No. US20050032165A1
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/816,011
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-57

Query Match          96.0%; Score 2007; DB 17; Length 426;
Best Local Similarity 94.9%; Pred. No. 1.2e-181;
Matches 390; Conservative 13; Mismatches 8; Indels 0; Gaps 0;
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Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255
Qy 241 AIYFVWITLTITGFDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300
Db 256 AIYFVWITLTITGFDHVGAGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGRLVRVIS 315
Qy 301 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRLSAELAGNHQ 360
Db 316 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRLSAELAGNHQ 375
Qy 361 ELTPCRRTLSVNHLTSERDVLPLLKTESIYLNGLTPHCAGEDIAVIENMK 411
Db 376 ELTPCRRTLSVNHLTSERDVLPLLKTESIYLNGLAPHCAGEIAVIENIK 426

RESULT 14
US-10-870-492-60
; Sequence 60, Application US/10870492
; Publication No. US20050032165A1
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/816,011
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 60
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-60

Query Match 95.8%; Score 2003; DB 17; Length 426;
Best Local Similarity 94.9%; Pred. No. 2.9e-181;
Matches 390; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MAAPDLDPKSAQNSKPLSFSTKPTVLASRVESDSAINVMKTKVSTIFLVVLYLII 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 16 VAAPDLDPKSAQNSKPLSFSTKPTVLASRVESDTTINVMKTKVSTIFLVVLYLII 75
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 GAAVFKALEQPOEISORTTIVIKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 GATVFKALEQPEHSISQRTTIVIKQTFISQHSVCNSTELDELIQIIVAAINAGIIPLGNT 135
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 SNQSHWDLGSSFFPAGTVITTTIGFNIISPRTEGKIFCIIYALLGIPILFGFLLAGVGQ 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 136 SNQISHWDLGSSFFPAGTVITTTIGFNIISPRTEGKIFCIIYALLGIPILFGFLLAGVGQ 195
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 241 AIYFVWITLTITGFDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 256 AIYFVWITLTITGFDHVGAGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGRLVRVIS 315
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 301 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRLSAELAGNHQ 360
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 316 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRLSAELAGNHQ 375
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 361 ELTPCRRTLSVNHLTSERDVLPLLKTESIYLNGLTPHCAGEDIAVIENMK 411
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 376 ELTPCRRTLSVNHLTSERDVLPLLKTESIYLNGLAPHCAGEIAVIENIK 426
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Search completed: July 13, 2005, 09:07:01
Job time : 91.2442 secs

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Db 376 ELTPCRRTLSVNHLTSERDVLPLLKTESIYLNGLAPHCAGEIAVIENIK 426

RESULT 15
US-10-870-492-59
; Sequence 59, Application US/10870492
; Publication No. US20050032165A1.
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/816,011
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 59
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-59

Query Match 95.8%; Score 2002; DB 17; Length 426;
Best Local Similarity 94.6%; Pred. No. 3.6e-181;
Matches 389; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MAAPDLDPKSAQNSKPLSFSTKPTVLASRVESDSAINVMKTKVSTIFLVVLYLII 60
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Db 16 VAAPDLDPKSAQNSKPLSFSTKPTVLASRVESDTTINVMKTKVSTIFLVVLYLII 75
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 61 GAAVFKALEQPOEISORTTIVIKQTFIAQACVNSTELDELIQIIVAAINAGIIPLGNS 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 76 GATVFKALEQPEHSISQRTTIVIKQTFISQHSVCNSTELDELIQIIVAAINAGIIPLGNT 135
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 121 SNQSHWDLGSSFFPAGTVITTTIGFNIISPRTEGKIFCIIYALLGIPILFGFLLAGVGQ 180
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 136 SNQISHWDLGSSFFPAGTVITTTIGFNIISPRTEGKIFCIIYALLGIPILFGFLLAGVGQ 195
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 241 AIYFVWITLTITGFDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 256 AIYFVWITLTITGFDHVGAGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGRLVRVIS 315
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 301 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRLSAELAGNHQ 360
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 316 KKTKEVGEFRAHAAEWANTVAEFKETRRLRSVEIYDKFORATSVKRLSAELAGNHQ 375
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 361 ELTPCRRTLSVNHLTSERDVLPLLKTESIYLNGLTPHCAGEDIAVIENMK 411
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 376 ELTPCRRTLSVNHLTSERDVLPLLKTESIYLNGLAPHCAGEIAVIENIK 426
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:10:49 ; Search time 26.3635 Seconds
(without alignments)
1163.760 Million cell updates/sec

Title: US-09-503-089A-4
Perfect score: 2090
Sequence: 1 MAAPDLLDPKSAQNSKPRL.....LNGLTPHCAGEDIAVIENMK 411

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2084	99.7	411	3	US-09-236-080-6
2	2044	97.8	411	3	US-09-236-080-2
3	2044	97.8	411	3	US-09-336-643A-83
4	1855	88.8	370	3	US-09-144-914-8
5	1251.5	59.9	538	4	US-09-949-016-7001
6	1251.5	59.9	558	4	US-09-949-016-7368
7	797	38.1	393	4	US-09-432-470-2
8	797	38.1	393	4	US-09-432-470-4
9	797	38.1	419	4	US-09-949-016-6913
10	797	38.1	440	4	US-09-949-016-7809
11	551	26.4	107	3	US-09-236-080-4
12	420	20.1	499	4	US-09-561-763-2
13	420	20.1	499	4	US-09-431-367B-2
14	392	18.8	361	4	US-09-362-842-14
15	387	18.5	332	4	US-09-561-763-5
16	387	18.5	332	4	US-09-431-367B-5
17	376.5	18.0	336	3	US-08-749-816-2
18	376.5	18.0	336	3	US-09-144-914-2
19	370	17.7	394	3	US-09-144-914-4
20	345.5	16.5	388	4	US-09-949-016-7631
21	345	16.5	405	3	US-09-144-914-5
22	342	16.4	313	3	US-09-336-643A-81
23	342	16.4	313	4	US-09-561-763-8
24	342	16.4	313	4	US-09-431-367B-8
25	317.5	15.2	408	4	US-09-362-842-12
26	299.5	14.3	618	1	US-08-332-312-2
27	293	14.0	257	4	US-09-949-016-6654

28	293	14.0	273	4	US-09-949-016-7794	Sequence 7794, Ap
29	256.5	12.3	395	4	US-09-362-842-6	Sequence 6, Appli
30	219	10.4	336	1	US-08-332-312-4	Sequence 4, Appli
31	216.5	10.4	730	4	US-09-362-842-4	Sequence 4, Appli
32	216.5	10.4	741	4	US-09-362-842-67	Sequence 67, Appli
33	216.5	10.4	741	4	US-09-270-767-45442	Sequence 45442, A
34	212	10.1	401	4	US-09-561-763-11	Sequence 11, Appl
35	210.5	10.1	995	4	US-09-431-367B-11	Sequence 11, Appl
36	210.5	10.1	995	4	US-09-362-842-2	Sequence 2, Appli
37	184.5	8.8	383	3	US-08-749-816-4	Sequence 4, Appli
38	184.5	8.8	383	3	US-09-144-914-7	Sequence 7, Appli
39	172	8.2	1153	4	US-09-362-842-8	Sequence 8, Appli
40	160.5	7.7	347	3	US-08-749-816-3	Sequence 3, Appli
41	160.5	7.7	347	3	US-09-144-914-6	Sequence 6, Appli
42	152.5	7.3	197	3	US-09-336-643A-16	Sequence 16, Appli
43	141	6.7	146	4	US-09-362-842-69	Sequence 69, Appli
44	141	6.7	146	4	US-09-270-767-31685	Sequence 31685, A
45	128	6.1	988	4	US-09-614-480-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-236-080-6
; Sequence 6, Application US/092336080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-236-080-6

Query Match 99.7%; Score 2084; DB 3; Length 411;
Best Local Similarity 99.8%; Pred. No. 1.9e-210;
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MAAPDLLDPKSAQNSKPRLSPSSKPTVLASRVSDSAINVMKWTSTIFLWVLYLI	60
Db	1	MAAPDLLDPKSAQNSKPRLSPSSKPTVLASRVSDSAINVMKWTSTIFLWVLYLI	60
Qy	61	GAAPKALEPOEISORTTIVIQOTFIAQACVNSTELDELIQQIVAAGIIPLGNS	120
Db	61	GAAPKALEPOEISORTTIVIQOTFIAQACVNSTELDELIQQIVAAGIIPLGNS	120
Qy	121	SNQVSHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQ	180
Db	121	SNQVSHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIIYALLGIPLFGFLLAGVGQ	180
Qy	181	LGTIFGKGIKVEDTFIKWNVSQTKIRIISTITIFILFGCVLVALPAVFKHIEGWSALD	240
Db	181	LGTIFGKGIKVEDTFIKWNVSQTKIRIISTITIFILFGCVLVALPAVFKHIEGWSALD	240
Qy	241	AIYFVWITLTITIGFDYVAGGSDIEYLPYKPVWFWLVLGAYFAAVLSMIGDMURVIS	300
Db	241	AIYFVWITLTITIGFDYVAGGSDIEYLPYKPVWFWLVLGAYFAAVLSMIGDMURVIS	300
Qy	301	KTKKEVGEFRAHAAEWNTAETKERRRSLVSDYDKFORATSVKRLKSLAELAGNHQ	360
Db	301	KTKKEVGEFRAHAAEWNTAETKERRRSLVSDYDKFORATSVKRLKSLAELAGNHQ	360
Qy	361	ELTPCRTLNVNHLTSREVLPLPKASIIYINGLTPHCAGEDIAVIENMK	411
Db	361	ELTPCRTLNVNHLTSREVLPLPKASIIYINGLTPHCAGEDIAVIENMK	411

RESULT 2

US-09-236-080-2
; Sequence 2, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-2

Query Match 97.8%; Score 2044; DB 3; Length 411;
Best Local Similarity 96.4%; Pred. No. 3e-206;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAAPDLLDPKSAQNSKRLSPSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLI 60
Db 1 MAAPDLLDPKSAQNSKRLSPSTPTVLASRVSDTINVMKWTSTIFLVVLYLI 60

Qy 61 GAAVFKALEQPOEISQRTTIVIQOTFIAQHACVNSTELDELIQIIVAAINAGIPLGNS 120
Db 61 GATVFKALEQPEHISQRTTIVIQOTFISQSCVNSTELDELIQIIVAAINAGIPLGNT 120

Qy 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIYALLGIFLFGFLAGVGDQ 180
Db 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIYALLGIFLFGFLAGVGDQ 180

Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAVIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAVIFKHIEGWSALD 240

Qy 241 AIYFVVTITLTIGFGDYVAGSDIEYLDYFKPVVWFILVGLAYFAAVALSMIGDMLRVIS 300
Db 241 AIYFVVTITLTIGFGDYVAGSDIEYLDYFKPVVWFILVGLAYFAAVALSMIGDMLRVIS 300

Qy 301 KKTKEEVEGFRAHAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
Db 301 KKTKEEVEGFRAHAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360

Qy 361 ELTPCRRTLNVNHLTSERVLPLLKTESIYNGLTTPHCAGEDIAVIENMK 411
Db 361 ELTPCRRTLNVNHLTSERDLVPLLKTESIYNGLTTPHCAGEEIAVIENIK 411

RESULT 3

US-09-336-643A-83
; Sequence 83, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826

; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643A-83

Query Match 97.8%; Score 2044; DB 3; Length 411;
Best Local Similarity 96.4%; Pred. No. 3e-206;
Matches 396; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MAAPDLLDPKSAQNSKRLSPSSKPTVLASRVSDSAINVMKWTSTIFLVVLYLI 60
Db 1 MAAPDLLDPKSAQNSKRLSPSTPTVLASRVSDTINVMKWTSTIFLVVLYLI 60

Qy 61 GAAVFKALEQPOEISQRTTIVIQOTFIAQHACVNSTELDELIQIIVAAINAGIPLGNS 120
Db 61 GATVFKALEQPEHISQRTTIVIQOTFISQSCVNSTELDELIQIIVAAINAGIPLGNT 120

Qy 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIYALLGIFLFGFLAGVGDQ 180
Db 121 SNOVSHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIYALLGIFLFGFLAGVGDQ 180

Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAVIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAVIFKHIEGWSALD 240

Qy 241 AIYFVVTITLTIGFGDYVAGSDIEYLDYFKPVVWFILVGLAYFAAVALSMIGDMLRVIS 300
Db 241 AIYFVVTITLTIGFGDYVAGSDIEYLDYFKPVVWFILVGLAYFAAVALSMIGDMLRVIS 300

Qy 301 KKTKEEVEGFRAHAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360
Db 301 KKTKEEVEGFRAHAEWTANVTAEFKETRRRLSVEIYDKFORATSVKRLSAELAGNHQ 360

Qy 361 ELTPCRRTLNVNHLTSERVLPLLKTESIYNGLTTPHCAGEDIAVIENMK 411
Db 361 ELTPCRRTLNVNHLTSERDLVPLLKTESIYNGLTTPHCAGEEIAVIENIK 411

RESULT 4

US-09-144-914-8
; Sequence 8, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Pink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS. THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; EARLIER FILING DATE: 1996-02-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-144-914-8

*no answer there is
no answer?
or plug.*

Query Match 88.8%; Score 1855; DB 3; Length 370;

Best Local Similarity 99.5%; Pred. No. 2e-186;
Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MAAPDLLDPKSAQNSKPRLSFSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60
Db 1 MAAPDLLDPKSAQNSKPRLSFSKPTVLASRVESDSAINVMKWKTVSTIFLVVLYLII 60

Qy 61 GAAVFKALEQPOISQRTTIVIOKQTFIAQHACVNSTELDELIIQOIVAAINAGIIPLGNS 120
Db 61 GAAVFKALEQPOISQRTTIVIOKQTFIAQHACVNSTELDELIIQOIVAAINAGIIPLGNS 120

Qy 121 SNOVSHWDLGSSFFAGTWTITGFGNISPRTEGGKIFCIYALIGIPILEGFLAGVGDO 180
Db 121 SNOVSHWDLGSSFFAGTWTITGFGNISPRTEGGKIFCIYALIGIPILEGFLAGVGDO 180

Qy 181 LGTIFGKGIKAKVEDTFIKMNVSTQKIRIISTIFILFGCVLFVALPAVIEKHIEGWSALD 240
Db 181 LGTIFGKGIKAKVEDTFIKMNVSTQKIRIISTIFILFGCVLFVALPAVIEKHIEGWSALD 240

Qy 241 AIYFVWITLTIGFDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDLRVLIS 300
Db 241 AIYFVWITLTIGFDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDLRVLIS 300

Qy 301 KKTKEEVGEFRAHAAEWNTAEFKETRRLRSVEIYDKFORATSVKRLKSABLAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWNTAEFKETRRLRSVEIYDKFORATSVKRLKSABLAGNHQ 360

Qy 361 ELTPCRR 368
Db 361 ELTPCMT 368

RESULT 5
US-09-949-016-7001
; Sequence 7001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7001
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7001

Query Match 59.9%; Score 1251.5; DB 4; Length 538;
Best Local Similarity 64.3%; Pred. No. 1.1e-122;
Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;

Qy 2 AAPDLLDPKSA-----AQNKPRLSFSKPTVLASRVESDS---AINVMKWKTVSTI 50
Db 17 AAPVCQPKSATNGQPPAPAPTPTPLRSSRATVVA-RMEGTSQGLQTVMKKTVAI 75

Qy 51 FLVVLYLIIGAFAVKALEQPOISQRTTIVIOKQTFIAQHACVNSTELDELIIQOIVAAI 110
Db 76 FVVVVVYLVGTGLVFRALAEQPPESQKNTIALEKAEFLRDHVCVSPQLETLIHALDAD 135

Qy 111 NAGIIPLGNSNQVSHWDLGSSFFAGTWTITGFGNISPRTEGGKIFCIYALIGIPI 170
Db 136 NAGVSPIGNSSNNSHWDLGSAFFAGTWTITGFGNISPRTEGGKIFCIYALIGIPI 195

Qy 171 GFLLAGVGDLGTIFGKGIKAKVEDTFIKMNVSTQKIRIISTIFILFGCVLFVALPAVIF 230
Db 196 GFLLAGIGDQGLTIFGKSIARVEKVKRQKQVSTQKIRVISTIFILAGCIVFTIPAVIF 255

Qy 231 KHIEGWSALDAIYFVVVITLTITGFDYVAGG-SDIEYLDYKPVVWFWILVGLAYFAAVL 289
Db 256 KYIEGHTALESYFVVVVITLTITGFDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVL 315

Qy 290 SMIGDLRVLISKKTKEEVGEFRAHAAEWNTAEFKETRRLRSVEIYDKFORATSV--- 346
Db 316 SMIGDLRVLISKKTKEEVGEIKAHAAEWKANTAEFRETERRLSVEIHDKLQRAATIRSM 375

Qy 347 -KKLSAELAGNHQELTFCRRTL 369
Db 376 ERRRLGLDQRAHSLDMLSPKRSV 399

RESULT 6
US-09-949-016-7368
; Sequence 7368, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7368
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7368

Query Match 59.9%; Score 1251.5; DB 4; Length 558;
Best Local Similarity 64.3%; Pred. No. 1.2e-122;
Matches 247; Conservative 54; Mismatches 66; Indels 17; Gaps 5;

Qy 2 AAPDLLDPKSA-----AQNKPRLSFSKPTVLASRVESDS---AINVMKWKTVSTI 50
Db 37 AAPVCQPKSATNGQPPAPAPTPTPLRSSRATVVA-RMEGTSQGLQTVMKKTVAI 95

Qy 51 FLVVLYLIIGAFAVKALEQPOISQRTTIVIOKQTFIAQHACVNSTELDELIIQOIVAAI 110
Db 96 FVVVVVYLVGTGLVFRALAEQPPESQKNTIALEKAEFLRDHVCVSPQLETLIHALDAD 155

Qy 111 NAGIIPLGNSNQVSHWDLGSSFFAGTWTITGFGNISPRTEGGKIFCIYALIGIPI 170
Db 156 NAGVSPIGNSSNNSHWDLGSAFFAGTWTITGFGNISPRTEGGKIFCIYALIGIPI 215

Qy 171 GFLLAGVGDLGTIFGKGIKAKVEDTFIKMNVSTQKIRIISTIFILFGCVLFVALPAVIF 230
Db 216 GFLLAGIGDQGLTIFGKSIARVEKVKRQKQVSTQKIRVISTIFILAGCIVFTIPAVIF 275

Qy 231 KHIEGWSALDAIYFVVVITLTITGFDYVAGG-SDIEYLDYKPVVWFWILVGLAYFAAVL 289
Db 276 KYIEGHTALESYFVVVVITLTITGFDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVL 335

Qy 290 SMIGDLRVLISKKTKEEVGEFRAHAAEWNTAEFKETRRLRSVEIYDKFORATSV--- 346
Db 336 SMIGDLRVLISKKTKEEVGEIKAHAAEWKANTAEFRETERRLSVEIHDKLQRAATIRSM 395

Qy 347 -KKLSAELAGNHQELTFCRRTL 369
Db 396 ERRRLGLDQRAHSLDMLSPKRSV 419

RESULT 10
US-09-949-016-7809
; Sequence 7809, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7809
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7809

Query Match 38.1%; Score 797; DB 4; Length 440;
Best Local Similarity 51.1%; Pred. No. 5.3e-75;
Matches 145; Conservative 60; Mismatches 77; Indels 2; Gaps 1;
QY 42 MKWTKVSTFLVVLVLIIGAAVFKALQEQEISQRTTIVIQKOTFIAQHACVNSTELDE 101
DB MRSTLLALLLVLYVSGALVFRALQEPHQEQARELGEVREKFLRAHPCVSDQELGL 107
QY 102 LIQIIVAINAGIIPLGHNSSNOVSH--WDLGSSFFAGTIVTTIGFNGISPRTEGGKIFC 159
DB 108 LIKEVADALGGGADPETNSTSSHSADWDLGSAFFSGTIIITIGYGNVALRTDAGRLFC 167
QY 160 IYALLGLPLFGFLAGVDGLTIFGKIAKVEDTFIKWVSOQKIRIISTIFILFGC 219
DB 168 IFYALVGLPLGILLAGVDRGSSLRHGIGHIEAIFLKHVPPBLRVLSAMFLLLGC 227
QY 220 VLFVALPAVIFKHIEGWSALDAIYFVWITLTITIGFGDYVAGSDIEYLDYFKVPVWFIL 279
DB 228 LLFVLTPFVFCYMEDWSKLEAIYFVITVITVGVGDYVAGADPRQDSPAYQPLVWFIL 287
QY 280 VGLYFAAVLVMIGDMLRVISKTKKEVEGEFRAHAAEWNTAVTA 323
DB 288 LGLAYFASVLTITIGNWLRVSRTRAEIMGGLTAQAASWTGTVTA 331

RESULT 11
US-09-236-080-4
; Sequence 4, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-4

Query Match 26.4%; Score 551; DB 3; Length 107;
Best Local Similarity 100.0%; Pred. No. 4.7e-50;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 119 NSSQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIFLFGV 178
DB 1 NSSQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIFLFGV 60
QY 179 DQLGTIFGKIAKVEDTFIKWVSOQKIRIISTIFILFGCVLFVAL 225
DB 61 DQLGTIFGKIAKVEDTFIKWVSOQKIRIISTIFILFGCVLFVAL 107
RESULT 12
US-09-561-763-2
; Sequence 2, Application US/09561763
; Patent No. 6664373
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP2
; CURRENT APPLICATION NUMBER: US/09/561,763
; CURRENT FILING DATE: 2000-04-29
; PRIOR APPLICATION NUMBER: 09/431,367
; PRIOR FILING DATE: 01-11-1999
; PRIOR APPLICATION NUMBER: US 09/259,951
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-763-2

Query Match 20.1%; Score 420; DB 4; Length 499;
Best Local Similarity 30.8%; Pred. No. 3e-35;
Matches 105; Conservative 62; Mismatches 120; Indels 54; Gaps 11;
QY 54 VVLYIIGAAVFKALQEQEISQRTTIVIQKOTFIAQHACVNSTELDELIQOIVAAINAG 113
DB 12 IIFVLAIGAAIFVLEBEPHWEAKQVYVTKLHLKBPCLGQEGLDKILEVSDAAGQ 71
QY 114 IIPGNSNQVSHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIYIALLGIFLFGV 173
DB 72 VAITGNQT--FNNWNPAMIFAATVITIGYGNVAPKTPAGRLFCVYGLFGVPL--C 126
QY 174 LAGVDQGLTIFGKIAKVEDTFIKWVSOQKIRIISTIFILFGCVLFVALPAVIEKHI 233
DB 127 LTWI-SALGKFFGGRAKRLGQFLTKRGVSLRKAQTCTVIFVGVVHLVLPFPVFWT 185
QY 234 EGWSALDAIYFVWITLTITIGFGDYVAG--GSDIEYLDYFKVPVWFVILVGLAYFAA 292
DB 186 EGMVIEGLYYFITISTIGFGDFVAGVWNPANYHALYRYFVELMWILGLAW---LSLF 241
QY 293 GDWLRVSKTKKEVEGEFRAHAAEWNTAVTAETRRRLSRVIEYDKQRATSVRKL 352
DB 242 VNV-----KVSMP-----VEVHKAIKRRRR-----RKESF 267
QY 353 ELAGNHQELTPCRRITLNVHLTSEV--LPPLLKAESY 391
DB 268 E-SSPHS-----RRALQVKGSTASKOVNIFSLSKKEEY 301

RESULT 13
US-09-431-367B-2
; Sequence 2, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A.J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951

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OM protein - protein search, using sw model.

Run on: July 13, 2005, 07:58:54 ; Search time 101.398 Seconds
(without alignments)
1567.669 Million cell updates/sec

Title: US-09-503-089A-2
Perfect score: 2100
Sequence: 1 MAAPDLLDPKSAQNSKPKL.....LNLTPHCAGEIAVIENTIK 411

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2100	100.0	411	3	Aae10341 Human TRE
2	2095	99.8	411	2	Aay34133 Human pot
3	2095	99.8	411	2	Aay28496 h-TREK1 p
4	2095	99.8	411	4	Aab50044 Human TRE
5	2095	99.8	411	7	Adp03586 Human GPC
6	2095	99.8	411	8	Adq76698 Human two
7	2092	99.6	411	5	Aae16597 Human TWI
8	2089	99.5	422	7	Adp03575 Human GPC
9	2062	98.2	426	4	Aau07618 Human pot
10	2058	98.0	426	4	Aau07622 Human pot
11	2057	98.0	426	4	Aau07623 Human pot
12	2054	97.8	426	4	Aau07625 Human pot
13	2053	97.8	426	4	Aau07624 Human pot
14	2041	97.2	411	3	Aae10342 Murine TR
15	2035	96.9	411	2	Aay28497 Mouse h-T
16	1833	87.3	370	6	Aay30648 A mechani
17	1638.5	78.0	337	6	ABR41487 Human DIT
18	1243	59.2	538	5	Aab47930 Human TRE
19	1243	59.2	538	5	Aae16596 Human TWI
20	1243	59.2	538	5	ABP69333 Human pol
21	1243	59.2	543	5	Aae21804 Human TRE
22	1243	59.2	543	5	Aau81354 Human hum
23	1243	59.2	543	5	Aau79472 Human nov
24	1243	59.2	543	5	ABB83542 Hypothala
25	1243	59.2	543	6	ADA05746 Human NOV

26	1243	59.2	543	7	ADB08315	Ade08315 Novel pro
27	1243	59.2	543	8	ADN62910	Adn62910 Human NOV
28	1239	59.0	543	5	AAU79473	Aau79473 Human nov
29	1215.5	57.9	724	5	AAO14193	Aao14193 Human tra
30	988	47.0	228	8	ADJ27190	Adj27190 Human TRI
31	803	38.2	392	6	ABU60891	Abu60891 Human G p
32	803	38.2	393	3	AAy94426	Aay94426 Human h-T
33	803	38.2	393	3	AAy94425	Aay94425 Human h-T
34	803	38.2	393	4	AAAG6777	Aag67777 Human mec
35	803	38.2	419	5	AAAG78406	Aag78406 Amino aci
36	803	38.2	419	7	Aae38597	Aae38597 Human pot
37	803	38.2	419	7	ADK52550	Adk52550 Hematolog
38	803	38.2	419	8	ADH51639	Adh51639 Human 123
39	803	38.2	419	8	ADI27936	Adi27936 Human TWI
40	803	38.2	419	8	ADR44894	Adr44894 Polypepti
41	803	38.2	1314	4	AAU04571	Aau04571 Human G-p
42	803	38.2	1314	6	ABU60872	Abu60872 Human G p
43	776.5	37.0	398	2	AAV30647	Aay30647 A mechani
44	768.5	36.6	398	5	AAE16598	Aae16598 Human TWI
45	636	30.3	383	4	ABG02731	Abg02731 Novel hum

ALIGNMENTS

RESULT 1
AAE10341
ID AAE10341 standard; protein; 411 AA.
XX
AC AAE10341;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human TREK-1 potassium channel protein.
XX
KW Human; potassium channel protein; TREK-1; anaesthetic; analgesia;
KW amnesia.
XX
OS Homo sapiens.
XX
PN WO200047738-A2.
XX
PD 17-AUG-2000.
XX
PF 11-FEB-2000; 2000WO-IB000226.
XX
PR 12-FEB-1999; 99US-0119727P.
PR 11-FEB-2000; 2000US-00503089.
(CNRS) CNRS CENT NAT RECH SCI.
Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;
WPI; 2000-549146/50.
N-PSDB; AAD17496.
Novel nucleic acid encoding a TREK-1 potassium channel protein for
transfecting cells to be used to identify compounds with anesthetic
properties.
Claim 3; Page 28; 39pp; English.
The invention relates to human and mouse TREK-1 potassium channel
proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
useful for transfecting cells to induce expression of the TREK-1
potassium channel protein. These cells are then used in assays to
identify compounds which have anaesthetic properties, producing a safe,
reversible state of unconsciousness with concurrent amnesia and analgesia
in a mammal upon inhalation. The present sequence is human TREK-1
potassium channel protein
Sequence 411 AA;

Query Match 100.0%; Score 2100; DB 3; Length 411;
 Best Local Similarity 100.0%; Pred. No. 8.e-210;
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60
 |||||
 DB 1 MAAPDLLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60
 |||||

QY 61 GATVFKALEQHPHEISORTTIVIKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120
 |||||
 DB 61 GATVFKALEQHPHEISORTTIVIKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120
 |||||

QY 121 SNOISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIVALLGIPFLGELLAGVGQ 180
 |||||
 DB 121 SNOISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIVALLGIPFLGELLAGVGQ 180
 |||||

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240
 |||||
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240
 |||||

QY 241 AIYFVVIITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300
 |||||
 DB 241 AIYFVVIITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300
 |||||

QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRLRSVEIYDKFORATSIKRKLSAELAGNHQ 360
 |||||
 DB 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRLRSVEIYDKFORATSIKRKLSAELAGNHQ 360
 |||||

QY 361 ELTPCRRTLSVNLHTNERDVLPLLKTESIYLNGLTPHCAGEEIAVNIENIK 411
 |||||
 DB 361 ELTPCRRTLSVNLHTNERDVLPLLKTESIYLNGLTPHCAGEEIAVNIENIK 411
 |||||

RESULT 2
 AAY34133
 ID AAY34133 standard; protein; 411 AA.
 XX
 AC AAY34133;
 XX
 DT 30-NOV-1999 (first entry)
 XX
 DE Human potassium channel K+Hnov59.
 XX
 KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
 KW cardiovascular disorder; CNS disorder; renal disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO9943696-A1.
 XX
 PD 02-SEP-1999.
 XX
 PF 22-FEB-1999; 99WO-US003826.
 XX
 PR 25-FEB-1998; 98US-0076687P.
 PR 07-AUG-1998; 98US-0095836P.
 PR 19-JAN-1999; 99US-0116448P.
 XX
 PA (AXYS-) AXYS PHARM INC.
 XX
 PI Miller AP, Curran ME, Hu P, Rutter M, Wang J;
 XX
 DR WPI; 1999-527591/44.
 DR N-PSDB; AA211915.
 XX
 PT New nucleic acids encoding mammalian K+Hnov potassium channel proteins,
 PT useful for the diagnosis and treatment of episodic ataxia with myokymia,
 PT cardiac arrhythmia, epilepsy and Bartter's syndrome.
 XX
 PS Claim 3; Page 104-105; 112pp; English.
 XX
 CC This sequence represents the human K+Hnov59 potassium channel. K+Hnov
 CC proteins have a high degree of homology to known potassium channels and

CC may be alpha subunits, which form the functional channel, or accessory
 CC subunits that act to modulate the channel activity. K+Hnov59 is a 4
 CC transmembrane domain, 2 pore domain potassium channel. The gene is
 CC located on chromosome 19, determined via PCR chromosomal localisation
 CC using primers AA211939 and AA211940. K+Hnov cDNAs were isolated by
 CC extension of expressed sequence tags (ESTs) which were related but not
 CC identical to known human potassium channels. Potential polymorphisms
 CC detected as sequence variants between multiple independent clones.
 CC Potassium channels have critical roles in various cell types and
 CC biochemical pathways. Defective potassium channels are known to cause
 CC four human diseases: episodic ataxia with myokymia; cardiac arrhythmia
 CC (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium
 CC channels are critical components of virtually all cells, it is likely
 CC that abnormal potassium channels are also implicated in certain renal,
 CC cardiovascular and central nervous system (CNS) disorders. Nucleotides
 CC encoding K+Hnov proteins may be used for identifying homologous or
 CC related proteins and the DNA sequences encoding them. They may be used to
 CC produce compositions that modulate the expression and function of the
 CC K+Hnov protein and in studying the biochemical pathways associated with
 CC it. They may also be used for the recombinant production of K+Hnov
 CC protein in fermentation cultures. Additionally, such nucleotides may be
 CC used in gene therapy protocols for the treatment of diseases associated
 CC with abnormal potassium channels
 XX
 SQ Sequence 411 AA;
 Query Match 99.8%; Score 2095; DB 2; Length 411;
 Best Local Similarity 99.8%; Pred. No. 2.9e-209;
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60
 |||||
 DB 1 MAAPDLLDPKSAQNSKPRLSFTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60
 |||||

QY 61 GATVFKALEQHPHEISORTTIVIKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120
 |||||
 DB 61 GATVFKALEQHPHEISORTTIVIKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120
 |||||

QY 121 SNOISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIVALLGIPFLGELLAGVGQ 180
 |||||
 DB 121 SNOISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIVALLGIPFLGELLAGVGQ 180
 |||||

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240
 |||||
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIFKHIEGWSALD 240
 |||||

QY 241 AIYFVVIITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300
 |||||
 DB 241 AIYFVVIITLTITIGFDYVAGGSDIEYLDYKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300
 |||||

QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRLRSVEIYDKFORATSIKRKLSAELAGNHQ 360
 |||||
 DB 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRLRSVEIYDKFORATSIKRKLSAELAGNHQ 360
 |||||

QY 361 ELTPCRRTLSVNLHTNERDVLPLLKTESIYLNGLTPHCAGEEIAVNIENIK 411
 |||||
 DB 361 ELTPCRRTLSVNLHTSERDVLPLLKTESIYLNGLTPHCAGEEIAVNIENIK 411
 |||||

RESULT 3
 AAY28496
 ID AAY28496 standard; protein; 411 AA.
 XX
 AC AAY28496;
 XX
 DT 12-OCT-1999 (first entry)
 XX
 DE h-TREK1 polypeptide.
 XX
 KW h-TREK1; two pore potassium channel; inflammatory disease;
 KW chromosome 1q32.
 XX
 OS Homo sapiens.

XX WO9937762-A1.
 XX
 XX
 XX 29-JUL-1999.
 XX
 XX 02-DEC-1998; 98WO-EP007805.
 XX
 XX 27-JAN-1998; 98EP-00300570.
 XX 09-OCT-1998; 98GB-00022135.
 XX
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Meadows HJ, Chapman CG;
 XX
 XX WPI; 1999-469126/39.
 XX N-PSDB; AA200039.
 XX
 XX New two pore potassium channel used for, e.g. treatment of cancer,
 XX pulmonary, cardiovascular and inflammatory diseases.
 XX
 XX Claim 3; Page 24; 44pp; English.
 XX
 XX This sequence is the h-TREK1 polypeptide, encoded by the h-TREK1
 XX polynucleotide AA200039. h-TREK1 is a two pore potassium channel, and the
 XX gene maps to human chromosome 1q32, between the markers D15237 and
 XX W15105. The polynucleotide sequence of h-TREK1 can be used to diagnose a
 XX disease or susceptibility to a disease related to expression or activity
 XX of h-TREK-1 polypeptides. The methods of diagnosis may be used in the
 XX treatment of diseases including cancer, pulmonary, cardiovascular, and
 XX inflammatory diseases, pain, psychiatric disorders including depression
 XX and schizophrenia, neurodegenerative diseases including Alzheimer's,
 XX stroke, and head trauma and neurological disorders including migraine
 XX
 XX Sequence 411 AA;

Query Match 99.8%; Score 2095; DB 2; Length 411;
 Best Local Similarity 99.8%; Pred. No. 2.9e-209;
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAPDLLDPKSAQNSKPRLSPTKPTVLASRVESDTTINVMKWKTSTIFLVVLYLII 60
 Db 1 MAAPDLLDPKSAQNSKPRLSPTKPTVLASRVESDTTINVMKWKTSTIFLVVLYLII 60
 QY 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIIVAAINAGIIPLGNT 120
 Db 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIIVAAINAGIIPLGNT 120
 QY 121 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIPFGFLLAGVGQ 180
 Db 121 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIPFGFLLAGVGQ 180
 QY 181 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHEGWSALD 240
 Db 181 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHEGWSALD 240
 QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWFVILVGLAYFAAVLSMIGDMLRVIS 300
 Db 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWFVILVGLAYFAAVLSMIGDMLRVIS 300
 QY 301 KTKKEVGFRAHAAEWNTANVTAEFKTRRRLSVEIYDKFORATSIRKRLSALAGNHQ 360
 Db 301 KTKKEVGFRAHAAEWNTANVTAEFKTRRRLSVEIYDKFORATSIRKRLSALAGNHQ 360
 QY 361 ELTPCRRTLSVNLHLSERDVLPLLLATSTIYLNGLTPHCAGREIAVNIENK 411
 Db 361 ELTPCRRTLSVNLHLSERDVLPLLLATSTIYLNGLTPHCAGREIAVNIENK 411

RESULT 4

AAB50044

ID AAB50044 standard; protein; 411 AA.

XX

AC AAB50044;

XX 19-MAR-2001 (first entry)
 XX Human TREK.
 XX
 XX Human; TREK; 2P domain potassium channel; resting membrane potential;
 XX neuronal excitability; neurotransmitter release modulation; epilepsy;
 XX neurological disorder; sleep-related disorder; cognitive dysfunction;
 XX attention deficit disorder; addiction; anxiety; phobia;
 XX Parkinson's chorea; Huntington's chorea; cerebral palsy; incontinence;
 XX erectile dysfunction; alopecia.
 XX
 XX Homo sapiens.
 XX
 XX WO200072863-A2.
 XX
 XX 07-DEC-2000.
 XX
 XX 01-JUN-2000; 2000WO-GB002107.
 XX
 XX 01-JUN-1999; 99GB-00012733.
 XX
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Hervieu GJ, Meadows HJ, Randall AD;
 XX
 XX WPI; 2001-080422/09.
 XX N-PSDB; AAC90412.
 XX
 XX Use of human TREK1 polypeptide, polynucleotides encoding them and
 XX modulators of h-TREK1 polypeptides for treating epilepsy, sleep-related
 XX disorders, addiction and dyskinesias including Parkinson's and
 XX Huntington's chorea.
 XX
 XX Claim 7; Page 29; 35pp; English.

Query Match 99.8%; Score 2095; DB 4; Length 411;
 Best Local Similarity 99.8%; Pred. No. 2.9e-209;
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAPDLLDPKSAQNSKPRLSPTKPTVLASRVESDTTINVMKWKTSTIFLVVLYLII 60
 Db 1 MAAPDLLDPKSAQNSKPRLSPTKPTVLASRVESDTTINVMKWKTSTIFLVVLYLII 60
 QY 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIIVAAINAGIIPLGNT 120
 Db 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSCVNSTELDELIQQIIVAAINAGIIPLGNT 120
 QY 121 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIPFGFLLAGVGQ 180
 Db 121 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYVALLGIPFGFLLAGVGQ 180
 QY 181 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHEGWSALD 240
 Db 181 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHEGWSALD 240
 QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWFVILVGLAYFAAVLSMIGDMLRVIS 300
 Db 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVFWFVILVGLAYFAAVLSMIGDMLRVIS 300

hand done
 (FR)

QY 301 KKTKEVGEFRAHAEWTANTVAEPKTRRRLSVEIYDKFORATSIKKRLSIAELAGNHQ 360
 |||||
 Db 301 KKTKEVGEFRAHAEWTANTVAEPKTRRRLSVEIYDKFORATSIKKRLSIAELAGNHQ 360
 |||||
 QY 361 ELTPCRRRLTSVNLHNTNRDVLPLPKTESIYNGLTTPHCAGEIAVIENIK 411
 |||||
 Db 361 ELTPCRRRLTSVNLHNTNRDVLPLPKTESIYNGLTTPHCAGEIAVIENIK 411
 |||||

RESULT 5

ADP03586

ID ADP03586 standard; protein; 411 AA.

XX

AC ADP03586;

XX

DT 29-JUL-2004 (first entry)

XX

DE Human GPCR potassium channel, subfamily K, member 2 protein.

XX

KW GPCR, G-protein coupled receptor; neuroprotective; nootropic;
 KW tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant;
 KW anticonvulsant; antiparkinsonian; cytotatic; cardiac; hypotensive;
 KW analgesic; anorectic; anti-HIV; antiaesthmic; osteopathic;
 KW uropathic; antitumor; antiallergic; cell cycle regulation; neurological;
 KW severe mental retardation; dyskinesia; brain; spinal cord; affective;
 KW neoplastic; cardiovascular; immunological; immune; endocrinal; growth;
 KW eating; HIV infection; cancer; metabolic; pituitary;
 KW chromosome identification; gene therapy; human; receptor;
 KW potassium channel subfamily K member 2.

XX

OS Homo sapiens.

XX

PN WO2003062393-A2.

XX

PD 31-JUL-2003.

XX

XX 22-JAN-2003; 2003WO-US001911.

PF

XX 22-JAN-2002; 2002US-0350724P.

PR

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX

XX Ramanathan CS, Gopal S, Mintier G, Feder JN;

XX

XX WPI; 2003-618283/58.

XX

PT New nucleic acid molecule encoding a human G-protein coupled receptor,
 PT useful for diagnosing, preventing or treating diseases involving the
 PT receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
 PT cancer.

XX

PS Example 1; SEQ ID NO 31; 224pp; English.

XX

XX The invention relates to a novel isolated GPCR (G-protein coupled
 CC receptor) nucleic acid molecule. The polynucleotide and polypeptide of
 CC the invention demonstrate neuroprotective, nootropic, tranquiliser.
 CC antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,
 CC antiparkinsonian, cytotatic, cardiac, hypotensive, antianigmal,
 CC analgesic, anorectic, anti-HIV, antiaesthmic, osteopathic, uropathic,
 CC antitumor and antiallergic properties. The nucleic acid molecule and
 CC polypeptide of the invention may be useful in diagnosing, preventing,
 CC treating or ameliorating a medical condition, such as a disorder related
 CC to aberrant G-protein coupled signalling, a disorder related to aberrant
 CC cell cycle regulation, neurological disorders, severe mental retardation
 CC and dyskinesias, brain disorders, spinal cord disorders, affective
 CC disorders, neoplastic disorders, cardiovascular disorders, immunological
 CC disorders, immune-related disorders, endocrinal diseases, growth
 CC disorders, eating disorders, HIV infection, cancers, metabolic disorders
 CC and pituitary disorders. Furthermore, the polynucleotide may be used in
 CC chromosome identification, in identifying organisms from minute
 CC biological samples, in gene therapy or as a molecular weight marker. The
 CC current sequence is that of a human GPCR (G-protein coupled receptor)
 CC protein of the invention which was used for homology purposes.

XX Sequence 411 AA;
 SQ
 Query Match 99.8%; Score 2095; DB 7; Length 411;
 Best Local Similarity 99.8%; Pred. No. 2.9e-209;
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWKTSTIFLWVLYLII 60
 |||||
 Db 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWKTSTIFLWVLYLII 60
 |||||
 QY 61 GATVFKALEQPEHISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAINAGIIPLGNT 120
 |||||
 Db 61 GATVFKALEQPEHISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAINAGIIPLGNT 120
 |||||
 QY 121 SNQISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIVALLGIFLFGELLAGVGDO 180
 |||||
 Db 121 SNQISHWDLGSSFFPAGTVITTIIGFNGISPRTEGGKIFCIIVALLGIFLFGELLAGVGDO 180
 |||||
 QY 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTIFLFGCVLFVALPAIIFKHIEGWSALD 240
 |||||
 Db 181 LGTIFGKGIKVEDTFIKWVNSQTKIRIISTIFLFGCVLFVALPAIIFKHIEGWSALD 240
 |||||
 QY 241 AIYFVVIITLTITIGFGDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
 |||||
 Db 241 AIYFVVIITLTITIGFGDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDWLRVIS 300
 |||||
 QY 301 KKTKEVGEFRAHAEWTANTVAEPKTRRRLSVEIYDKFORATSIKKRLSIAELAGNHQ 360
 |||||
 Db 301 KKTKEVGEFRAHAEWTANTVAEPKTRRRLSVEIYDKFORATSIKKRLSIAELAGNHQ 360
 |||||
 QY 361 ELTPCRRRLTSVNLHNTNRDVLPLPKTESIYNGLTTPHCAGEIAVIENIK 411
 |||||
 Db 361 ELTPCRRRLTSVNLHNTNRDVLPLPKTESIYNGLTTPHCAGEIAVIENIK 411
 |||||

RESULT 6

ADQ76698

ID ADQ76698 standard; protein; 411 AA.

XX

AC ADQ76698;

XX

DT 07-OCT-2004 (first entry)

XX

XX Human two pore domain potassium channel TREK-1.

XX

XX TREK-1; sleep; two pore domain potassium channel; sedative; hypnotic;
 KW human.

XX

OS Homo sapiens.

XX

PN WO2004058325-A2.

XX

XX 15-JUL-2004.

XX

XX 23-DEC-2003; 2003WO-US040913.

XX

XX 23-DEC-2002; 2002US-0436201P.

XX

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX

XX Tononi G, Cirelli C;

XX

XX WPI; 2004-534024/51.

XX

XX GENBANK; NM014217.

XX

PT Identifying a Drosophila mutant fly with a no rebound, short sleep and/or
 PT no sleep deprivation resistant phenotype, for identifying sleep-related
 PT molecular targets, comprises recording sleep quantity of the mutant fly.

XX

PS Claim 12; SEQ ID NO 2; 83pp; English.

XX

XX The present sequence is that of the human two pore domain K+ channel TREK

CC -1. In rats, TREK-1 is highly expressed in much of the brain and is
 CC inhibited by protein kinase C and protein kinase C mediated
 CC phosphorylation. It is activated by volatile general anaesthetics and is
 CC expressed at high levels in the brain of sleep animals. Based on these
 CC criteria and on experimental results, it is hypothesized that TREK-1 is a
 CC key mediator of sleep (when open) and waking (when closed). The invention
 CC provides methods for identifying a sleep- or wakefulness-promoting
 CC compound based on the compound's ability to modulate two pore domain K+
 CC channels such as TREK-1. It also provides screening methods for isolating
 CC short sleep, no rebound and sleep deprivation resistant Drosophila
 CC mutants useful for identifying sleep-related molecular targets.

XX Sequence 411 AA;

Query Match 99.8%; Score 2095; DB 8; Length 411;
 Best Local Similarity 99.8%; Pred. No. 2.9e-209;
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60

DB 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60

QY 61 GATVFKALEOPHEISORTTIVIOKQTFISQHSVCNSTELDELIOQIVAAINAGIIPLGNT 120

DB 61 GATVFKALEOPHEISORTTIVIOKQTFISQHSVCNSTELDELIOQIVAAINAGIIPLGNT 120

QY 121 SNOIASHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVDQ 180

DB 121 SNOIASHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVDQ 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIPFKHIEGWSALD 240

DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIPFKHIEGWSALD 240

QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300

DB 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300

QY 301 KKTKEEVGFRAHAAEWNTANVTAEFKTRRRLSVEIYDKFORATSIKRKLASLGNHNO 360

DB 301 KKTKEEVGFRAHAAEWNTANVTAEFKTRRRLSVEIYDKFORATSIKRKLASLGNHNO 360

QY 361 ELTPCRTLTSVNLHTNDRDVLPLPKTESIYLNGLTPHCAGEBIAVNIENIK 411

DB 361 ELTPCRTLTSVNLHTNDRDVLPLPKTESIYLNGLTPHCAGEBIAVNIENIK 411

RESULT 7

AAE16597

ID AAE16597 standard; protein; 411 AA.

XX AAE16597;

XX 18-APR-2002 (first entry)

XX Human TWIK-Related K+ Channel-1 (TREK-1) protein.

XX Human; TWIK-Related K+ Channel-1; TREK-1; anaesthetic; screening.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 47..65

XX Domain /note= "M1 membrane spanning segment"

XX Region 127..150

XX Region /note= "P1 pore domain"

XX Region 158..178

XX Region /note= "M2 membrane spanning segment"

XX Region 209..230

XX Region /note= "M3 membrane spanning segment"

XX Domain 236..259

XX Region /note= "P2 pore domain"

XX Region 274..293

FT /note= "M4 membrane spanning segment"

XX WO200200715-A2.

XX 03-JAN-2002.

XX 27-JUN-2001; 2001WO-IB001436.

XX 27-JUN-2000; 2000US-0214559P.

XX 27-JUN-2001; 2001US-00892360.

XX (CNRS) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lesage F, Romey G;

XX WPI; 2002-139903/18.

XX New mammalian K+ channel protein with two pore domains, for screening

XX various compounds, particularly for identifying biologically active

XX compounds with anaesthetic properties.

XX Disclosure; Fig 1A; 50pp; English.

XX The invention relates to a mammalian K+ channel protein with two pore

XX domains, called TREK2 (TWIK-Related K+ Channel). The protein produces

XX currents whose current-voltage relationship is slightly inwardly

XX rectifying in high symmetrical K+ conditions. TREK2 is a member of the

XX fatty acid-activated and mechanosensitive K+ channel family. TREK-2 gene

XX located on chromosome 14q31 is abundantly expressed in kidney, pancreas

XX and moderately in testis, brain, colon and small intestine. The mammalian

XX K+ channel protein is useful in methods for screening various compounds.

XX In particular, the protein is useful in methods for identifying

XX biologically active compounds with anaesthetic properties. The present

XX sequence is TREK-1 protein used in the invention

XX Sequence 411 AA;

Query Match 99.6%; Score 2092; DB 5; Length 411;

Best Local Similarity 99.8%; Pred. No. 6e-209;

Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60

DB 1 MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTIFLVVLYLII 60

QY 61 GATVFKALEOPHEISORTTIVIOKQTFISQHSVCNSTELDELIOQIVAAINAGIIPLGNT 120

DB 61 GATVFKALEOPHEISORTTIVIOKQTFISQHSVCNSTELDELIOQIVAAINAGIIPLGNT 120

QY 121 SNOIASHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVDQ 180

DB 121 SNOIASHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFGFLLAGVDQ 180

QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIPFKHIEGWSALD 240

DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIPFKHIEGWSALD 240

QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300

DB 241 AIYFVVITLTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300

QY 301 KKTKEEVGFRAHAAEWNTANVTAEFKTRRRLSVEIYDKFORATSIKRKLASLGNHNO 360

DB 301 KKTKEEVGFRAHAAEWNTANVTAEFKTRRRLSVEIYDKFORATSIKRKLASLGNHNO 360

QY 361 ELTPCRTLTSVNLHTNDRDVLPLPKTESIYLNGLTPHCAGEBIAVNIENIK 411

DB 361 ELTPCRTLTSVNLHTNDRDVLPLPKTESIYLNGLTPHCAGEBIAVNIENIK 411

RESULT 8

ADP03575

ID ADP03575 standard; protein; 422 AA.

XX ADP03575;
AC
XX
DT 29-JUL-2004 (first entry)
DE
XX
DE Human GPCR twin pore channel" protein variant "Gene 9" protein.
XX
XX GPCR; G-protein coupled receptor; neuroprotective; nootropic;
KW tranquiliser; antimigraine; neuroleptic; antimanic; antidepressant;
KW anticonvulsant; antiparkinsonian; cytotstatic; cardiant; hypotensive;
KW antitanginal; analgesic; anorectic; anti-HIV; antiaethmatic; osteopathic;
KW uropathic; antituler; antiallergic; cell cycle regulation; neurological;
KW severe mental retardation; dyskinesia; brain; spinal cord; affective;
KW neoplastic; cardiovascular; immunological; immune; endocrinal; growth;
KW eating; HIV infection; cancer; metabolic; pituitary;
KW chromosome identification; gene therapy; human; receptor;
KW twin pore channel; potassium channel subfamily K member 2 variant.
XX
XX Homo sapiens.
XX
XX WO2003062393-A2.
XX
XX 31-JUL-2003.
XX
XX 22-JAN-2003; 2003WO-US001911.
XX
XX 22-JAN-2002; 2002US-0350724P.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Ramanathan CS, Gopal S, Mintier G, Feder JN;
XX
XX WPI; 2003-618283/58.
DR N-PSDB; ADP03564.
XX
XX New nucleic acid molecule encoding a human G-protein coupled receptor,
PT useful for diagnosing, preventing or treating diseases involving the
PT receptor, e.g. Parkinson's disease, dementia, asthma, hypertension or
PT cancer.
XX
XX Claim 5; SEQ ID NO 20; 224pp; English.
XX
XX The invention relates to a novel isolated GPCR (G-protein coupled
CC receptor) nucleic acid molecule. The polynucleotide and polypeptide of
CC the invention demonstrate neuroprotective, nootropic, tranquiliser,
CC antimigraine, neuroleptic, antimanic, antidepressant, anticonvulsant,
CC antiparkinsonian, cytotstatic, cardiant, hypotensive, antitanginal,
CC analgesic, anorectic, anti-HIV, antiaethmatic, osteopathic, uropathic,
CC antituler and antiallergic properties. The nucleic acid molecule and
CC polypeptide of the invention may be useful in diagnosing, preventing,
CC treating or ameliorating a medical condition, such as a disorder related
CC to aberrant G-protein coupled signalling, a disorder related to aberrant
CC cell cycle regulation, neurological disorders, severe mental retardation
CC and dyskinesias, brain disorders, spinal cord disorders, affective
CC disorders, neoplastic disorders, cardiovascular disorders, immunological
CC disorders, immune-related disorders, endocrinal diseases, growth
CC disorders, eating disorders, HIV infection, cancers, metabolic disorders
CC and pituitary disorders. Furthermore, the polynucleotide may be used in
CC chromosome identification, in identifying organisms from minute
CC biological samples, in gene therapy or as a molecular weight marker. The
CC current sequence is that of a human GPCR (G-protein coupled receptor),
CC protein which was isolated by the method of the invention.
XX
XX Sequence 422 AA;
XX
Query Match 99.5%; Score 2089; DB 7; Length 422;
Best Local Similarity 99.3%; Pred. No. 1.3e-208;
Matches 408; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
1 MAAPDLLDPKSAQNSKPLRSFTKPTVLASRVESDTTINVMKKTSTVIFLWVLYLI 60
12 LAAPDLLDPKSAQNSKPLRSFTKPTVLASRVESDTTINVMKKTSTVIFLWVLYLI 71

QY 61 GATVFKALEQPEHISQRTTIVIQKTFISQHSQSVNSTELDELIQOIVAAINAGIIPLGNT 120
DB 72 GATVFKALEQPEHISQRTTIVIQKTFISQHSQSVNSTELDELIQOIVAAINAGIIPLGNT 131
QY 121 SNQISHWDLGSSFPFAGTVITTTIGFNGISPRTEGGKIFCIIYVALLGIPLFGFLAGVGQ 180
DB 132 SNQISHWDLGSSFPFAGTVITTTIGFNGISPRTEGGKIFCIIYVALLGIPLFGFLAGVGQ 191
QY 181 LGTIFGKGIKVEDPFIKWNYSQTKIRIISTITIFLFGCVLFPALPFIKHEGWSALD 240
DB 192 LGTIFGKGIKVEDPFIKWNYSQTKIRIISTITIFLFGCVLFPALPFIKHEGWSALD 251
QY 241 AIYFVVIITLTITGFDYVAGGSDIEYDFYKPVVFWFLLVGLYFAAVALSMIGDMLRVIS 300
DB 252 AIYFVVIITLTITGFDYVAGGSDIEYDFYKPVVFWFLLVGLYFAAVALSMIGDMLRVIS 311
QY 301 KKTKEEVGEFRAHAAEWNTAETPKETRRRLSVBIYDKFQKQATSIKRLSLAELAGNHQ 360
DB 312 KKTKEEVGEFRAHAAEWNTAETPKETRRRLSVBIYDKFQKQATSIKRLSLAELAGNHQ 371
QY 361 ELTPCRRLTSVNHLTNRDVLPLPKTESIYVINGLTPHCAGEEIAVIENIK 411
DB 372 ELTPCRRLTSVNHLTNRDVLPLPKTESIYVINGLTPHCAGEEIAVIENIK 422
RESULT 9
AAU07618
ID AAU07618 standard; protein; 426 AA.
XX
XX AAU07618;
XX
XX 21-NOV-2001 (first entry)
XX
XX Human potassium ion channel TPKC1 protein.
XX
XX Transmembrane potassium ion channel protein; inward potassium flux;
KW pest control; membrane potential; pesticide; antihelminthic; nematode;
KW insect; TPKC1; human.
XX
XX Homo sapiens.
XX
XX WO200161006-A2.
XX
XX 23-AUG-2001.
XX
XX 14-FEB-2001; 2001WO-US004680.
XX
XX 15-FEB-2000; 2000US-00503849.
XX
XX (BADI) BASF CORP.
XX
XX Pausch MH;
XX
XX WPI; 2001-536570/59.
XX
XX N-PSDB; AAS12169.
XX
XX New polypeptide, a mutant potassium ion channel protein for improving
PT inward potassium flux under acidic conditions.
XX
XX Example 15; Page 45; 131pp; English.
XX
XX The invention relates to a mutant potassium ion channel protein, having
CC four membrane spanning domains and two pore forming domains, comprising a
CC mutation at the second pore forming domain. The expression of the mutant
CC protein in a cell confers improved inward potassium flux and the ability
CC to grow in the presence of potassium. Mutant proteins and their
CC corresponding polynucleotide sequences can therefore be used to improve
CC inward potassium flux into cells under acidic conditions by modulating
CC the membrane potential using therapeutic agents. The sequences may be
CC used to develop agonists and antagonists of potassium channel proteins in
CC order to control pests such as nematodes and insects. This sequence
CC represents a human transmembrane potassium ion channel protein, TPKC1
XX

SQ Sequence 426 AA;
 Query Match 98.2%; Score 2062; DB 4; Length 426;
 Best Local Similarity 98.5%; Pred. No. 8.5e-206;
 Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSPTKPTVLASRVESDTTINVMKKTSTVFILVWVLYLI 60
 DB 16 VAAPDLLDPKSAQAQNSKPRLSPTKPTVLASRVESDTTINVMKKTSTVFILVWVLYLI 75
 QY 61 GATVPKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 120
 DB 76 GATVPKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 135
 QY 121 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 180
 DB 136 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 195
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
 DB 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 255
 QY 241 AIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDLVRVIS 300
 DB 256 AIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDLVRVIS 315
 QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360
 DB 316 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 375
 QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIEAVIENIK 411
 DB 376 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIEAVIENIK 426

RESULT 10
 AAU07622
 ID AAU07622 standard; protein; 426 AA.
 AC AAU07622;
 DT 21-NOV-2001 (first entry)
 DE Human potassium ion channel TPKC1 mutant protein #1.
 KW Transmembrane potassium ion channel protein; inward potassium flux;
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;
 KW insect; TPKC1; human; mutant; mutein.
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 256
 FT /note= "wild-type Ala replaced by Thr"
 XX
 XX WO200161006-A2.
 XX
 XX 23-AUG-2001.
 XX
 XX 14-FEB-2001; 2001WO-US004680.
 XX
 XX 15-FEB-2000; 2000US-00503849.
 XX
 XX (BADI) BASF CORP.
 XX
 XX Pausch MH;
 XX
 XX WPI; 2001-536570/59.
 XX
 XX N-PSDB; AAS12181.
 XX
 XX New polypeptide, a mutant potassium ion channel protein for improving
 XX inward potassium flux under acidic conditions.

PS Claim 37; Page 113-115; 131pp; English.
 XX The invention relates to a mutant potassium ion channel protein, having a four membrane spanning domains and two pore forming domains, comprising a mutation at the second pore forming domain. The expression of the mutant protein in a cell confers improved inward potassium flux and the ability to grow in the presence of potassium. Mutant proteins and their corresponding polynucleotide sequences can therefore be used to improve inward potassium flux into cells under acidic conditions by modulating the membrane potential using therapeutic agents. The sequences may be used to develop agonists and antagonists of potassium channel proteins in order to control pests such as nematodes and insects. This sequence represents a human transmembrane potassium ion channel TPKC1 mutant protein
 XX
 XX Sequence 426 AA;
 SQ

Query Match 98.0%; Score 2058; DB 4; Length 426;
 Best Local Similarity 98.3%; Pred. No. 2.2e-205;
 Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQAQNSKPRLSPTKPTVLASRVESDTTINVMKKTSTVFILVWVLYLI 60
 DB 16 VAAPDLLDPKSAQAQNSKPRLSPTKPTVLASRVESDTTINVMKKTSTVFILVWVLYLI 75
 QY 61 GATVPKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 120
 DB 76 GATVPKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELIQQIVAAINAGIIPLGNT 135
 QY 121 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 180
 DB 136 SNOISHWDLGSSFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGQ 195
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
 DB 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 255
 QY 241 AIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDLVRVIS 300
 DB 256 TIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDLVRVIS 315
 QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360
 DB 316 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 375
 QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIEAVIENIK 411
 DB 376 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEIEAVIENIK 426

RESULT 11
 AAU07623
 ID AAU07623 standard; protein; 426 AA.
 XX
 XX AAU07623;
 XX
 XX 21-NOV-2001 (first entry)
 XX
 XX Human potassium ion channel TPKC1 mutant protein #2.
 XX
 XX Transmembrane potassium ion channel protein; inward potassium flux;
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;
 KW insect; TPKC1; human; mutant; mutein.
 XX
 XX Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 272
 FT /note= "wild-type Tyr replaced by His"
 XX
 XX WO200161006-A2.
 XX
 XX 23-AUG-2001.

XX 14-FEB-2001; 2001WO-US004680.
PF 15-FEB-2000; 2000US-00503849.
XX (BADI) BASF CORP.
XX Pausch MH;
PI WPI; 2001-536570/59.
XX N-PSDB; AAS12182.
DR New polypeptide, a mutant potassium ion channel protein for improving
PT inward potassium flux under acidic conditions.
XX Claim 37; Page 115-117; 131pp; English.
XX The invention relates to a mutant potassium ion channel protein, having
CC four membrane spanning domains and two pore forming domains, comprising a
CC mutation at the second pore forming domain. The expression of the mutant
CC protein in a cell confers improved inward potassium flux and the ability
CC to grow in the presence of potassium. Mutant proteins and their
CC corresponding polynucleotide sequences can therefore be used to improve
CC inward potassium flux into cells under acidic conditions by modulating
CC the membrane potential using therapeutic agents. The sequences may be
CC used to develop agonists and antagonists of potassium channel proteins in
CC order to control pests such as nematodes and insects. This sequence
CC represents a human transmembrane potassium ion channel TPKC1 mutant
CC protein
XX
SQ Sequence 426 AA;
Query Match 98.0%; Score 2057; DB 4; Length 426;
Best Local Similarity 98.3%; Pred. No. 2.8e-205;
Matches 404; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLSRVESDTTINVMKWTSTIFLVVLYLII 60
DB 16 VAAPDLLDPKSAQNSKPRLSFSTKPTVLSRVESDTTINVMKWTSTIFLVVLYLII 75
QY 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCVNSTELDELIQIIVAAINAGIIPLGNT 120
DB 76 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCVNSTELDELIQIIVAAINAGIIPLGNT 135
QY 121 SNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYVALLGIPLFGFLLAGVGQD 180
DB 136 SNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYVALLGIPLFGFLLAGVGQD 195
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHIEGWSALD 240
DB 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHIEGWSALD 255
QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVWFILVGLAYFAAIVLSMIGDLVRVIS 300
DB 256 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVWFILVGLAYFAAIVLSMIGDLVRVIS 315
QY 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVSEIYDKFQRTATSIKKKLSAELAGNHQ 360
DB 316 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVSEIYDKFQRTATSIKKKLSAELAGNHQ 375
QY 361 ELTPCRRTLNVNHLTSDRVLPPLKTESIYINGLTPHCAGBEIAVIENIK 411
DB 376 ELTPCRRTLNVNHLTSDRVLPPLKTESIYINGLTPHCAGBEIAVIENIK 426
RESULT 12
AAU07625
ID AAU07625 standard; protein; 426 AA.
XX
AC AAU07625;
XX
DT 21-NOV-2001 (first entry)
XX

DE Human potassium ion channel TPKC1 mutant protein #4.
XX Transmembrane potassium ion channel protein; inward potassium flux;
KW pest control; membrane potential; pesticide; antihelminthic; nematode;
KW insect; TPKC1; human; mutant; mutein.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Misc-difference 270
FT /note= "Wild-type Gly replaced by Arg"
XX WO200161006-A2.
XX PD 23-AUG-2001.
XX 14-FEB-2001; 2001WO-US004680.
XX 15-FEB-2000; 2000US-00503849.
XX (BADI) BASF CORP.
XX Pausch MH;
XX WPI; 2001-536570/59.
XX N-PSDB; AAS12184.
XX New polypeptide, a mutant potassium ion channel protein for improving
PT inward potassium flux under acidic conditions.
XX Claim 37; Page 119-120; 131pp; English.
XX The invention relates to a mutant potassium ion channel protein, having
CC four membrane spanning domains and two pore forming domains, comprising a
CC mutation at the second pore forming domain. The expression of the mutant
CC protein in a cell confers improved inward potassium flux and the ability
CC to grow in the presence of potassium. Mutant proteins and their
CC corresponding polynucleotide sequences can therefore be used to improve
CC inward potassium flux into cells under acidic conditions by modulating
CC the membrane potential using therapeutic agents. The sequences may be
CC used to develop agonists and antagonists of potassium channel proteins in
CC order to control pests such as nematodes and insects. This sequence
CC represents a human transmembrane potassium ion channel TPKC1 mutant
CC protein
XX
SQ Sequence 426 AA;
Query Match 97.8%; Score 2054; DB 4; Length 426;
Best Local Similarity 98.3%; Pred. No. 5.8e-205;
Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLSRVESDTTINVMKWTSTIFLVVLYLII 60
DB 16 VAAPDLLDPKSAQNSKPRLSFSTKPTVLSRVESDTTINVMKWTSTIFLVVLYLII 75
QY 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCVNSTELDELIQIIVAAINAGIIPLGNT 120
DB 76 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVCVNSTELDELIQIIVAAINAGIIPLGNT 135
QY 121 SNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYVALLGIPLFGFLLAGVGQD 180
DB 136 SNQISHWDLGSSFFPAGTVITTTIGFNGISPRTEGGKIFCIIYVALLGIPLFGFLLAGVGQD 195
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHIEGWSALD 240
DB 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFLFGCVLFVALPAIFKHIEGWSALD 255
QY 241 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVWFILVGLAYFAAIVLSMIGDLVRVIS 300
DB 256 AIYFVVITLTITGFGDYVAGGSDIEYLDYKPVVWFILVGLAYFAAIVLSMIGDLVRVIS 315
QY 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVSEIYDKFQRTATSIKKKLSAELAGNHQ 360

Db 316 KKTKEVGEFRAHAEWTANTVAEFKETRRRLSVSEIYDKFORATSIKRKLSAELAGNHQ 375
 QY 361 ELTPCRRTLSVNLHNTNEDVLPPLKTESIYLNGLTPHCAGBEIAVIENIK 411
 Db 376 ELTPCRRTLSVNLHNTSERDVLPLKTESIYLNGLAPHCAGBEIAVIENIK 426

RESULT 13
 AAU07624
 ID AAU07624 standard; protein; 426 AA.
 XX
 AC AAU07624;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Human potassium ion channel TPKC1 mutant protein #3.
 XX
 KW Transmembrane potassium ion channel protein; inward potassium flux;
 KW pest control; membrane potential; pesticide; antihelminthic; nematode;
 KW insect; TPKC1; human; mutant; muten.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 272 /note= "Wild-type Tyr replaced by His"
 FT Misc-difference 274 /note= "Wild-type Ala replace by Val"
 FT
 XX
 PN WO200161006-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 14-FEB-2001; 2001WO-US004680.
 XX
 PR 15-FEB-2000; 2000US-00503849.
 XX
 PA (BADI) BASF CORP.
 XX
 PI Pausch MH;
 XX
 XX WPI; 2001-536570/59.
 DR N-PSDB; AAS12183.
 XX
 PT New polypeptide, a mutant potassium ion channel protein for improving
 PT inward potassium flux under acidic conditions.
 XX
 PS Claim 37; Page 117-119; 131pp; English.
 XX
 CC The invention relates to a mutant potassium ion channel protein, having
 CC four membrane spanning domains and two pore forming domains, comprising a
 CC mutation at the second pore forming domain. The expression of the mutant
 CC protein in a cell confers improved inward potassium flux and the ability
 CC to grow in the presence of potassium. Mutant proteins and their
 CC corresponding polynucleotide sequences can therefore be used to improve
 CC inward potassium flux into cells under acidic conditions by modulating
 CC the membrane potential using therapeutic agents. The sequences may be
 CC used to develop agonists and antagonists of potassium channel proteins in
 CC order to control pests such as nematodes and insects. This sequence
 CC represents a human transmembrane potassium ion channel TPKC1 mutant
 CC protein
 XX
 SQ Sequence 426 AA;

Query Match 97.8%; Score 2053; DB 4; Length 426;
 Best Local Similarity 98.1%; Pred. No. 7.4e-205;
 Matches 403; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTIFLWVLYLII 60
 Db 16 VAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWTSTIFLWVLYLII 75
 QY 61 GATVFKALEQPHEISQRTTIVIQKQTFISQHSVCVNSTELDELIQQIVAAINAGIPLGNT 120

Db 76 GATVFKALEQPHEISQRTTIVIQKQTFISQHSVCVNSTELDELIQQIVAAINAGIPLGNT 135
 QY 121 SNQISHWDLGSSFFPAGTVTTTIGFNGNISPRTEGKIFCIIYALLGIPFLGFLAGVGQ 180
 Db 136 SNQISHWDLGSSFFPAGTVTTTIGFNGNISPRTEGKIFCIIYALLGIPFLGFLAGVGQ 195
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
 Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255
 QY 241 AIYFVVITLTITIGFGDVVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGDMLRVIS 300
 Db 256 AIYFVVITLTITIGFGDVVAGGSDIEYLDIFYKPVVFWILVGLAYFAAVLSMIGRLRVIS 315
 QY 301 KKTKEVGEFRAHAEWTANTVAEFKETRRRLSVSEIYDKFORATSIKRKLSAELAGNHQ 360
 Db 316 KKTKEVGEFRAHAEWTANTVAEFKETRRRLSVSEIYDKFORATSIKRKLSAELAGNHQ 375
 QY 361 ELTPCRRTLSVNLHNTNEDVLPPLKTESIYLNGLTPHCAGBEIAVIENIK 411
 Db 376 ELTPCRRTLSVNLHNTSERDVLPLKTESIYLNGLAPHCAGBEIAVIENIK 426

RESULT 14
 AAE10342
 ID AAE10342 standard; protein; 411 AA.
 XX
 AC AAE10342;
 XX
 DT 10-DEC-2001 (first entry)
 XX
 DE Murine TREK-1 potassium channel protein.
 XX
 KW Murine; potassium channel protein; TREK-1; anaesthetic; analgesia;
 KW amnesia.
 XX
 OS Mus musculus.
 XX
 PN WO200047738-A2.
 XX
 PD 17-AUG-2000.
 XX
 PF 11-FEB-2000; 2000WO-IB000226.
 XX
 PR 12-FEB-1999; 99US-0119727P.
 PR 11-FEB-2000; 2000US-00503089.
 XX
 PA (CNRS) CNRS CENT NAT RECH SCI.
 XX
 PI Lazdunski M, Honore E, Lesage F, Romey G, Patel AJ;
 XX
 DR WPI; 2000-549146/50.
 DR N-PSDB; AAD17497.
 XX
 PT Novel nucleic acid encoding a TREK-1 potassium channel protein for
 PT transfecting cells to be used to identify compounds with anesthetic
 PT properties.
 XX
 PS Claim 9; Page 32-33; 39pp; English.
 XX
 CC The invention relates to human and mouse TREK-1 potassium channel
 CC proteins and their corresponding DNA molecules. TREK-1 nucleic acid is
 CC useful for transfecting cells to induce expression of the TREK-1
 CC potassium channel protein. These cells are then used in assays to
 CC identify compounds which have anaesthetic properties, producing a safe,
 CC reversible state of unconsciousness with concurrent amnesia and analgesia
 CC in a mammal upon inhalation. The present sequence is murine TREK-1
 CC potassium channel protein
 XX
 SQ Sequence 411 AA;

Query Match 97.2%; Score 2041; DB 3; Length 411;

[illegible]

CC diseases including cancer, pulmonary, cardiovascular, and inflammatory
 CC diseases, pain, psychiatric disorders including depression and
 CC schizophrenia, neurodegenerative diseases including Alzheimer's, stroke,
 CC and head trauma and neurological disorders including migraine
 XX Sequence 411 AA;
 SQ

Search completed: July 13, 2005, 08:39:46
Job time : 105.398 secs

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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:01:55 ; Search time 93.9622 Seconds
(without alignments)
2239.886 Million cell updates/sec

Title: US-09-503-089A-2

Perfect score: 2100

Sequence: 1 MAAPDLDDPKSAQNSKPLR.....LNLTPHCAGEIAVNIENIK 411

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2095	99.8	411	2 Q9NRT2	Q9nrt2 homo sapien
2	2079	99.0	411	2 Q8HY88	Q8hy88 bos taurus
3	2062	98.2	426	1 CIW2 HUMAN	Q95069 homo sapien
4	2042	97.2	414	2 Q6P6F9	Q6p6f9 mus musculus
5	2041	97.2	411	1 CIW2 MOUSE	P97438 mus musculus
6	2025	96.4	426	2 Q920B6	Q920b6 rattus norv
7	1254	59.7	538	2 Q6Q834	Q6q834 cryctolagus
8	1250	59.5	453	2 Q8B2B0	Q8b2b0 m mus muscu
9	1249.5	59.5	535	2 Q8BUW1	Q8buw1 m mus muscu
10	1249	59.5	538	1 CIW4_RAT	Q9j184 rattus norv
11	1243	59.2	538	1 CIW4 HUMAN	P57789 homo sapien
12	1243	59.2	543	2 Q6B014	Q6b014 homo sapien
13	1217.5	58.0	546	2 Q68Y11	Q68ey1 xenopus lae
14	803	38.2	393	1 CIW4 HUMAN	Q9nyg8 homo sapien
15	776.5	37.0	398	1 CIW4 MOUSE	Q8454 mus musculus
16	764.5	36.4	397	2 Q924I4	Q924i4 rattus norv
17	616	29.3	241	2 Q9CX88	Q9cx88 m mus muscu
18	516.5	24.6	152	2 Q6ZW95	Q6zww5 homo sapien
19	502.5	23.9	309	1 CIW6 HUMAN	Q96t55 homo sapien
20	496.5	23.6	294	2 Q6X6Z5	Q6x6z5 homo sapien
21	456	21.7	262	2 Q6X6Z3	Q6x6z3 homo sapien
22	450	21.4	322	2 Q6X6Z4	Q6x6z4 homo sapien
23	432.5	20.6	448	2 Q6PFU3	Q6ptf3 brachydanio
24	427	20.3	459	1 CIW5 HUMAN	Q95279 homo sapien
25	413	19.7	341	2 Q8HZT2	Q8hzt2 bos taurus
26	412.5	19.6	502	2 Q9JK62	Q9jk62 m potassium
27	409.5	19.5	257	2 Q80XE0	Q80xe0 mus musculus
28	406.5	19.4	307	2 Q801T4	Q801t4 xenopus lae
29	400	19.0	184	2 Q8N4V5	Q8n4v5 homo sapien
30	393	18.7	332	1 CIW6 HUMAN	Q96t54 homo sapien
31	380	18.1	336	2 Q8R454	Q8r454 cavia porce

32	379.5	18.1	336	1 CIW1 HUMAN	O00180 homo sapien
33	378.5	18.0	336	2 Q9Z2T2	Q9z2t2 rattus norv
34	377.5	18.0	336	2 Q99L99	Q99l99 mus musculus
35	372	17.7	331	2 Q8AVI5	Q8avi5 xenopus lae
36	370.5	17.6	336	1 CIW1 MOUSE	O08581 mus musculus
37	363	17.3	394	1 CIW3_HUMAN	O14649 homo sapien
38	357.5	17.0	365	1 CIW9_CAVPO	Q9j158 cavia porce
39	356.5	17.0	259	2 O02821	O02821 cryctolagus
40	355	16.9	323	2 Q6PE11	Q6pei1 brachydanio
41	351.5	16.7	396	2 Q923V6	Q923v6 rattus norv
42	349.5	16.6	374	1 CIW9 HUMAN	Q9ncp2 homo sapien
43	348.5	16.6	374	2 Q63ZIO	Q63zi0 xenopus lae
44	348	16.6	313	1 CIW6_HUMAN	Q9y237 homo sapien
45	347.5	16.5	330	1 CIW6_HUMAN	Q9h427 homo sapien

ALIGNMENTS

RESULT 1

Q9NRT2 PRELIMINARY; PRT; 411 AA.

AC Q9NRT2; DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)

DE Two-pore domain potassium channel TREK-1 (Potassium channel, subfamily K, member 2).

DE K, member 2).

GN Name=TREK-1; Synonyms=KCNK2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]_SEQUENCE FROM N.A.

RP TISSUE=Brain;

RC MEDLINE=20244931; PubMed=10784345;

RA Meadows H.J., Benham C.D., Cairns W., Gloger I.S., Jennings C., Medhurst A.D., Murdock P., Chapman C.G.;

RA "Cloning, localisation and functional expression of the human orthologue of the TREK-1 potassium channel."

RT Pfluegers Arch. 439:714-722(2000).

RL [2]_SEQUENCE FROM N.A.

RN TISSUE=PCR rescued clones;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grummond J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP [3]_SEQUENCE FROM N.A.

RN TISSUE=PCR rescued clones;

RA Strausberg R.;

RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.1.8) family.

DR EMBL; AF171068; AAF89743.1; --
 DR EMBL; BC069462; RAH69462.1; --
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0005267; F:potassium channel activity; IEA.
 DR GO; GO:0006811; F:ion transport; IEA.
 DR GO; GO:0005267; F:potassium channel activity; IEA.
 DR GO; GO:0006811; F:ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR003280; K+channel_2pore.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003976; K+channel_2pore.
 DR InterPro; IPR003976; K+channel_pore.
 DR PRINTS; PRO1333; 2POREKCHANEL.
 DR PRINTS; PRO1499; TREKCHANEL.
 DR PRINTS; PRO1333; 2POREKCHANEL.
 DR PRINTS; PRO1499; TREKCHANEL.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 411 AA; 45494 MW; FDE40CAB21B42A1C CRC64;

Query Match 99.8%; Score 2095; DB 2; Length 411;
 Best Local Similarity 99.8%; Pred. No. 1.7e-133;
 Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVESDTTINVMKKTSTIFLAVVLYLII 60
 DB 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVESDTTINVMKKTSTIFLAVVLYLII 60
 QY 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVNSTELDELIQIIVAAINAGIPLGNT 120
 DB 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVNSTELDELIQIIVAAINAGIPLGNT 120
 QY 121 SNQISHWDLGSSFFPAGTVITIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDD 180
 DB 121 SNQISHWDLGSSFFPAGTVITIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDD 180
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAIFKHIEGWSALD 240
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAIFKHIEGWSALD 240
 QY 241 AIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300
 DB 241 AIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300
 QY 301 KKTKEVGEFRAHAEWTANVTAEFKETRRRLSVEIYDKFORATSIKKRLSDELGNHQQ 360
 DB 301 KKTKEVGEFRAHAEWTANVTAEFKETRRRLSVEIYDKFORATSIKKRLSDELGNHQQ 360
 QY 361 ELTPCRRTLNVNHLNTERDVLPLKTESIYINGLTPHCAGEEIAVIENIK 411
 DB 361 ELTPCRRTLNVNHLNTERDVLPLKTESIYINGLTPHCAGEEIAVIENIK 411

RESULT 2
 Q8HY88 PRELIMINARY; PRT; 411 AA.
 AC Q8HY88
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Potassium channel subfamily K member 2.
 GN Name=Kcnk2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Adrenal cortex;
 RX MEDLINE=22370953; PubMed=12368289; DOI=10.1074/jbc.M207233200;
 RA Enyeart J.J., Xu L., Danthi S., Enyeart J.A.;
 RT "An ACTH- and ATP-regulated background K+ channel in adrenocortical
 cells is TREK-1";
 RL J. Biol. Chem. 277:49186-49199(2002).
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
 (TC 1.A.1.8) family.
 CC EMBL; AV148474; AAN37591.1; --

DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005216; F:ion channel activity; IEA.
 DR GO; GO:0005267; F:potassium channel activity; IEA.
 DR GO; GO:0006811; F:ion transport; IEA.
 DR GO; GO:0006813; P:potassium ion transport; IEA.
 DR InterPro; IPR003280; K+channel_2pore.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003976; K+channel_2pore.
 DR InterPro; IPR003976; K+channel_pore.
 DR PRINTS; PRO1333; 2POREKCHANEL.
 DR PRINTS; PRO1499; TREKCHANEL.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 411 AA; 45438 MW; A185EAC20A68CCDC CRC64;

Query Match 99.0%; Score 2079; DB 2; Length 411;
 Best Local Similarity 99.0%; Pred. No. 2e-132;
 Matches 407; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVESDTTINVMKKTSTIFLAVVLYLII 60
 DB 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVESDTTINVMKKTSTIFLAVVLYLII 60
 QY 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVNSTELDELIQIIVAAINAGIPLGNT 120
 DB 61 GATVFKALEQPEHEISQRTTIVIQKQTFISQHSVNSTELDELIQIIVAAINAGIPLGNT 120
 QY 121 SNQISHWDLGSSFFPAGTVITIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDD 180
 DB 121 SNQISHWDLGSSFFPAGTVITIGFNGISPRTEGGKIFCIIYALLGIPFLGFLAGVGDD 180
 QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAIFKHIEGWSALD 240
 DB 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIFILFGCVLFVALPAIFKHIEGWSALD 240
 QY 241 AIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300
 DB 241 AIYFVVITLTITIGFDYVAGGSDIEYDFYKPVWFWILVGLAYFAAVLSMIGDWLRVIS 300
 QY 301 KKTKEVGEFRAHAEWTANVTAEFKETRRRLSVEIYDKFORATSIKKRLSDELGNHQQ 360
 DB 301 KKTKEVGEFRAHAEWTANVTAEFKETRRRLSVEIYDKFORATSIKKRLSDELGNHQQ 360
 QY 361 ELTPCRRTLNVNHLNTERDVLPLKTESIYINGLTPHCAGEEIAVIENIK 411
 DB 361 ELTPCRRTLNVNHLNTERDVLPLKTESIYINGLTPHCAGEEIAVIENIK 411

RESULT 3
 CIW2 HUMAN
 ID CIW2 HUMAN STANDARD; PRT; 426 AA.
 AC Q95069; Q9UNE3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Potassium channel subfamily K member 2 (Outward rectifying potassium
 channel protein TREK-1) (TREK-1 K+ channel subunit) (Two-pore
 potassium channel TPCK1).
 DE Name=KCNK2; Synonyms=TREK, TREK1;
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
 RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
 RT "Inhalational anesthetics activate two-pore-domain background K+
 channels";
 RL Nat. Neurosci. 2:422-426(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Price L.A., Hellings S.E., Hayashi J.H., Pausch M.H.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Outward rectifying potassium channel.
 CC -!- SUBUNIT: Homodimer (Potential).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- MISCELLANEOUS: Activated by volatile general anaesthetics such as
 CC chloroform, halothane and isoflurane.
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
 CC (TC 1.A.1.8) family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; AF129399; RAD47569.1; --
 CC EMBL; AF004711; AD01203.1; --
 CC Genew; HGNC:6277; KCNK2.
 CC MIM; 603219; --
 CC GO; GO:0016020; C:membrane; NAS.
 CC GO; GO:0015271; F:outward rectifier potassium channel activity; NAS.
 CC GO; GO:0008813; P:potassium ion transport; NAS.
 CC InterPro; IPR003280; K+channel_2pore.
 CC InterPro; IPR001622; K+channel_pore.
 CC InterPro; IPR003976; Trek channel.
 CC PRINTS; PR01333; 2POREKCHANEL.
 CC PRINTS; PR01499; TREKCHANNEL.
 CC Glycoprotein; ion transport; Ionic channel; Potassium;
 CC Potassium channel; Transmembrane; Transport; Voltage-gated channel.
 KW DOMAIN 1 61 Cytoplasmic (Potential).
 FT TRANSMEM 62 82 Potential.
 FT DOMAIN 144 170 Pore-forming 1 (Potential).
 FT TRANSMEM 172 192 Potential.
 FT DOMAIN 193 223 Cytoplasmic (Potential).
 FT TRANSMEM 224 244 Potential.
 FT DOMAIN 253 283 Pore-forming 2 (Potential).
 FT TRANSMEM 288 308 Potential.
 FT DOMAIN 309 426 Essential for chloroform and halothane
 FT sensitivity (By similarity).
 FT DOMAIN 354 426 Required for basal channel activity (By
 FT similarity).
 FT CARBOHYD 110 110 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 134 134 N-linked (GlcNAc. .) (Potential).
 FT CONFLICT 2 16 Missing (in Ref. 2).
 FT CONFLICT 309 311 RLV -> DWL (in Ref. 2).
 FT CONFLICT 391 391 S -> N (in Ref. 2).
 FT CONFLICT 411 411 A -> T (in Ref. 2).
 FT SEQUENCE 426 AA; 47016 MW; 2ABA2336D4009F4E CRC64;
 SQ
 Query Match 98.2%; Score 2062; DB 1; Length 426;
 Best Local Similarity 98.5%; Pred. No. 3e-131;
 Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKKTSTVIFLVVLYLI 60
 DB :|||||
 QY 16 VMAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKKTSTVIFLVVLYLI 75
 DB :|||||
 QY 61 GATVFKALQEPHEISQRTTIVIQKQTFISQHSVCNSTELDELIQIIVAAINAGIIPLGNT 120
 DB 76 GATVFKALQEPHEISQRTTIVIQKQTFISQHSVCNSTELDELIQIIVAAINAGIIPLGNT 135
 QY 121 SNOISHWDLGSSFFPAGTIVITTFGNISPRTEGGKIFLCIIYALLGPIPLFGLLAGVGQD 180
 DB 136 SNOISHWDLGSSFFPAGTIVITTFGNISPRTEGGKIFLCIIYALLGPIPLFGLLAGVGQD 195
 QY 181 LGTIFGKIAKVEDTIFKNVSTKIRIISTIFILFGCVLFGVALPAIIFKHIEGWSALD 240
 DB 196 LGTIFGKIAKVEDTIFKNVSTKIRIISTIFILFGCVLFGVALPAIIFKHIEGWSALD 255
 QY 241 AIYFVVTITLTIGFDYVAGGSDIEYLDYKPVVFWFVILVGLAYFAANVLSMIGRLVRVIS 300
 DB :|||||

Db 256 AIYFVVTITLTIGFDYVAGGSDIEYLDYKPVVFWFVILVGLAYFAANVLSMIGRLVRVIS 315
 QY 301 KKTKEEVEGFRAHAAEWNTANVTAEPKTRRLSVIYDKFQRTATSIKRLKSLAELAGNHQ 360
 Db :|||||
 QY 316 KKTKEEVEGFRAHAAEWNTANVTAEPKTRRLSVIYDKFQRTATSIKRLKSLAELAGNHQ 375
 Db :|||||
 QY 361 ELTPCRRTLSVNNHLTNRDVLPLPKTESIYINGLTTPHCAGEEIAVIENIK 411
 Db 376 ELTPCRRTLSVNNHLTNRDVLPLPKTESIYINGLTTPHCAGEEIAVIENIK 426
 Db :|||||
 RESULT 4
 Q6P6P9
 ID Q6P6P9 PRELIMINARY; PRT; 414 AA.
 AC Q6P6P9;
 DT 05-JUL-2004 (TREMELrel. 27, Created)
 DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
 DE Kcnk2 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP -SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Ustin T.B., Toshivuk S., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RC Strausberg R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
 CC (TC 1.A.1.8) family.
 DR EMBL; BC062094; AAH62094.1; --
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.
 DR GO; GO:0005249; P:voltage-gated potassium channel activity; IDA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IDA.
 DR GO; GO:0006813; P:potassium ion transport; IDA.
 DR GO; GO:0030322; P:stabilization of membrane potential; TAS.
 DR InterPro; IPR003280; K+channel_2pore.
 DR InterPro; IPR001622; K+channel_pore.
 DR InterPro; IPR003976; Trek channel.
 DR PRINTS; PR01333; 2POREKCHANEL.
 DR PRINTS; PR01499; TREKCHANNEL.
 KW Ion transport; Ionic channel; Transmembrane; Transport.
 SQ SEQUENCE 414 AA; 45555 MW; 27F52D51DFPC66F8 CRC64;

Query Match 97.2%; Score 2042; DB 2; Length 414;
 Best Local Similarity 96.1%; Pred. No. 6.5e-130;
 Matches 395; Conservative 13; Mismatches 3; Indels 0; Gaps 0;


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Db      361 ELTPCRTLNVNLTSTREVLPLLKAEIYLNGLTTPHCAGEDIAVIENWK 411

RESULT 6
Q920B6
ID      Q920B6      PRELIMINARY;      PRT;      426 AA.
AC      Q920B6;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      2p domain potassium channel: KCNK2 (Tandem pore domain potassium
DE      channel TREK-1) (Arachidonic acid sensitive tandem pore domain
DE      potassium channel).
GN      Name=Kcnk2;
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=21219399; PubMed=11319556;
RA      Bockenhauer D., Zilberberg N., Goldstein S.A.;
RT      "KCNK2: reversible conversion of a hippocampal potassium leak into a
RT      voltage-dependent channel.";
RL      Nat. Neurosci. 4:486-491(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Wistar;
RX      MEDLINE=21896087; PubMed=11897938;
RA      Gu W., Schlichtchortl G., Hirsch J.R., Engels H., Karschin C.,
RA      Karschin A., Derst C., Steinlein O.K., Daut J.;
RT      "Expression pattern and functional characteristics of two novel splice
RT      variants of the two-pore-domain potassium channel TREK-2.";
RL      J. Physiol. 539:657-668(2002).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Wistar;
RX      MEDLINE=21896087; PubMed=11897938;
RA      Gu W., Schlichtchortl G., Hirsch J.R., Engels H., Karschin C.,
RA      Karschin A., Derst C., Steinlein O.K., Daut J.;
RT      "Expression pattern and functional characteristics of two novel splice
RT      variants of the two-pore-domain potassium channel TREK-2.";
RL      J. Physiol. 539:657-668(2002).

Query Match      96.4%; Score 2025; DB 2; Length 426;
Best Local Similarity 95.4%; Pred. No. 9.4e-129;
Matches 392; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY      1 MAAPDLLDPKSAQAQNSKPLSFTKPTVLASRVESDTTINVMKWTSTIFLVVLYLI 60
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      16 VAAPDLLDPKSAQAQNSKPLSFTKPTVLASRVESDTTINVMKWTSTIFLVVLYLI 75
QY      61 GATVPKALPQPEISORTTIVIQKOTFISQHSVNSTELDELIQIIVAINAGIPLGNT 120
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      76 GATVPKALPQPEISORTTIVIQKQNFIAQACVNSTELDELIQIIVAINAGIPLGNN 135
QY      121 SNOISHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIIVALLGIPFLGAGVQD 180
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      136 SNOVSHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIIVALLGIPFLGAGVQD 195
QY      181 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIFILFGCVLFVALPAIFPKHIEGWSALD 240

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Db      196 LGTIFGKGIAKVEDTFIKWNVSQTKIRIISTIFILFGCVLFVALPAIFPKHIEGWSALD 255
QY      241 AIYFVVITLTITGFDYVAGGSDIEYLDYKPKVWFWFVWILVGLYFAAVLSMIGDWLRVIS 300
Db      256 AIYFVVITLTITGFDYVAGGSDIEYLDYKPKVWFWFVWILVGLYFAAVLSMIGDWLRVIS 315
QY      301 KITKEVGEFRAHAAEWNTANTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360
Db      316 KITKEVGEFRAHAAEWNTANTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 375
QY      361 ELTPCRTLNVNLTSTREVLPLLKAEIYLNGLTTPHCAGEDIAVIENIK 411
Db      376 ELTPCRTLNVNLTSTREVLPLLKAEIYLNGLTTPHCAGEDIAVIENWK 426

RESULT 7
Q6Q834
ID      Q6Q834      PRELIMINARY;      PRT;      538 AA.
AC      Q6Q834;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Potassium channel TREK-2.
GN      Name=KCNK10;
OS      Oryctolagus cuniculus (Rabbit).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX      NCBI_TaxID=9986;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      Rae J.L.;
RA      Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC      (TC 1.A.1.8) family.
DR      EMBL; AY553324; AAC66991.1; -.
DR      GO; GO:0016021; C:integral to membrane; IEA.
DR      GO; GO:0005216; F:ion channel activity; IEA.
DR      GO; GO:0005267; F:potassium channel activity; IEA.
DR      GO; GO:0006811; P:ion transport; IEA.
DR      GO; GO:0006813; P:potassium ion transport; IEA.
DR      InterPro; IPR003280; K+channel_2pore.
DR      InterPro; IPR001622; K+channel_pore.
DR      InterPro; IPR003976; TREK channel.
DR      PRINTS; PR01333; 2POREKCHANEL.
DR      PRINTS; PR01499; TREKCHANEL.
KW      Ion transport; Ionic channel.
SQ      SEQUENCE 538 AA; 59844 MW; 1F06C8EA0DE8CB4D CRC64;

Query Match      59.7%; Score 1254; DB 2; Length 538;
Best Local Similarity 63.7%; Pred. No. 1.4e-76;
Matches 247; Conservative 56; Mismatches 63; Indels 22; Gaps 6;

QY      2 AAPDLLDPKSAQAQNSKPLSFTKPTVLASRVESDTTINVMKWTSTIFLVVLYLI 56
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      23 AAPVPCQPKSATNGHPAPRLSISRAVTVA-RMEGTSGQSQSVNMKWTVAIFVWV 81
QY      57 YLIIGATVPKALPQPEISORTTIVIQKOTFISQHSVNSTELDELIQIIVAINAGIIP 116
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      82 YLVTGGLVFRALPQPESSQKNTALEKAEFRDHCIVSPQLETLIQLADADNAGVSP 141
QY      117 LGNTSNQISHWDLGSSFFAGTIVITIGFNGISPRTEGGKIFCIIVALLGIPFLGAG 176
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      142 ICGNSNNSHWDLGSAFFAGTIVITIGYGNIAPTTEGGKIFCIILYFAIFGIPFLGAG 201
QY      177 VCDQLGTIFGKIAKVEDTFIKWNVSQTKIRIISTIFILFGCVLFVALPAIFPKHIEGW 236
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      202 IGDQLGTIFGKIAKVEDTFIKWNVSQTKIRIISTIFILFGCVLFVALPAIFPKHIEGW 261
QY      237 SALDAIYFVWITLTITGFDYVAGG-SDIEYLDYKPKVWFWFVWILVGLYFAAVLSMIGDW 295
Db      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      262 TALESIYFVWITLTITGFDYVAGG-SDIEYLDYKPKVWFWFVWILVGLYFAAVLSMIGDW 321
QY      296 LRVISKTKKEEYGEFRAHAAEWNTANTAEFKETRRRLSVEIYDKFORATSIKRKLSAELA 355

```


DE 10 (OUTWARD RECTIFYING POTASSIUM CHANNEL PROTEIN TREK-2) (TREK-2 K+ CHANNEL SUBUNIT) homolog.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;

RA Carninci P., Hayashizaki Y.;

RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

[2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA RIKEN FANTOM Consortium;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

[3]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RA The FANTOM Consortium;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

[4]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;

RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

RT "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";

RL Genome Res. 10:1617-1630(2000).

[5]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsuura T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohata E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

[6]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Cerebellum;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayaehida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the two pore domain potassium channel (TC 1.A.1.8) family.

CC EMBL: AK082153; BAC38424.1; -.

DR GO: GO:0016021; C:integral to membrane; IEA.

DR GO: GO:0005216; F:ion channel activity; IEA.

DR GO: GO:0005267; F:potassium channel activity; IEA.

DR GO: GO:0006911; P:ion transport; IEA.

DR GO: GO:0006913; P:potassium ion transport; IEA.

DR InterPro: IPR003280; K+channel_2pore.

DR InterPro: IPR001622; K+channel_pore.

DR InterPro: IPR003976; Trek channel.

DR PRINTS: PR01333; 2POREKCHANNEL.

DR PRINTS: PR01499; TREKCHANNEL.

KW ion transport; ionic channel; Transmembrane; Transport.

SQ SEQUENCE 535 AA; 59401 MW; 3E9BE89F875C26BD CRC64;

Query Match 59.5%; Score 1249.5; DB 2; Length 535;

Best Local Similarity 59.3%; Pred. No. 2.8e-76;

Matches 252; Conservative 61; Mismatches 77; Indels 35; Gaps 7;

QY 2 AAPDLLDPKSA--AQNSKRLSPSTKPTVLASVESDT---TINVNMKTKVTSTIFLVVL 56

DB 20 AAPVCPQKSAATNGHPVRLSISRATVVA-RMEGASQGLQTVMKWKTVAIFVWV 78

QY 57 YLIIGATVPKALEOPHEISORTTIVIOKOTFFISOHSCVNSTDELIIQIIVAINAGIIP 116

DB 79 YLVGTGLVFRALQEPFESSQKNTIALEKAEFLRDHICVSPQELDTIIQHALDADNAGVSP 138

QY 117 LGNTSNOISHWDLGSSFFAGTVITIGFNTISPRTEGGKIFCIIYALLGIPLFGLLAG 176

DB 139 VGNSSNSSSHWDLGSAFFAGTVITIGYNTAPSTEGGKIFCIIYALFIPFGFLLAG 198

QY 177 VGDQLGTIFKGIKVEDTFIKMNVSTQKIRIISTIFILFGCVLFPALIPKHIKHEGW 236

DB 199 IGDQLGTIFGKSIARVEKVRKQVSTQKIRVISTIFILAGCIVFTVPAVIFKIEGW 258

QY 237 SALDAIFYVVIITLTITGFGDYVAGG-SDIEYLDFFYQVWFWILVGLYPAAVLSMIGDW 295

DB 259 TALESIYFVVTLTITVFGDFVAGNAGINREYKPLVWFWILVGLYPAAVLSMIGDW 318

QY 296 LRVISKTEEVEGEPRAHAETANTVAFKPTRRLSVEIYDKFORATSI---KKKLS 351

DB 319 LRVLSKTEEVEGEIKAHAEKAVNTAFETRRRLSVEIHDKQRAATIRSMERRRLG 378

QY 352 AELAGNHNLTPCRRTL-----SVNHLTNERDVLPLPLKTESIYLNGLT 396

DB 379 LDQRAHSLDWLSPEKGSVFAALDTGRFKASSQESINRNPNLRLKGP-----EQLT 429

QY 397 PHCAG 401

DB 430 KEGQG 434

RESULT 10

CIWA RAT STANDARD; PRT; 538 AA.

ID CIWA RAT

AC 09JIS4;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 10 (Outward rectifying potassium channel protein TREK-2) (TREK-2 K+ channel subunit).

GN Names=Kcnk10; Synonyms=Trek2;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

[1]

SEQUENCE FROM N.A.

RX MEDLINE=20298807; PubMed=10747911; DOI=10.1074/jbc.M000445200;

RA Wang H., Kim Y., Kim D.;

RT TREK-2, a new member of the mechanosensitive tandem-pore K+ channel family.";

RL J. Biol. Chem. 275:17412-17419(2000).

CC -1- FUNCTION: Outward rectifying potassium channel. Produces rapidly activating and non-inactivating outward rectifier K(+) currents. Activated by arachidonic acid and other naturally occurring unsaturated free fatty acids.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: Expressed mainly in the cerebellum, spleen,

CC and testis.
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
 CC (TC 1.A.1.8) family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF196965; AAF75132.1; -;
 CC InterPro; IPR003280; K+channel_2pore.
 CC InterPro; IPR001622; K+channel_pore.
 CC InterPro; IPR003976; Trek_channel.
 CC PRINTS; PR01333; 2POREKCHANEL.
 CC PRINTS; PR01499; TREKCHANEL.
 CC Glycoprotein; Ion transport; Transmembrane; Transport; Potassium;
 CC Potassium channel; Transmembrane; Transport; Voltage-gated channel.
 CC DOMAIN 1 71 Cytoplasmic (Potential).
 CC TRANSMEM 72 92 Potential.
 CC DOMAIN 154 180 Pore-forming 1 (Potential).
 CC TRANSMEM 182 202 Potential.
 CC DOMAIN 203 233 Cytoplasmic (Potential).
 CC TRANSMEM 234 254 Potential.
 CC DOMAIN 263 294 Pore-forming 2 (Potential).
 CC TRANSMEM 299 319 Potential.
 CC DOMAIN 320 538 Cytoplasmic (Potential).
 CC CARBOHYD 144 144 N-linked (GlcNAc . .) (Potential).
 CC CARBOHYD 147 147 N-linked (GlcNAc . .) (Potential).
 CC SEQUENCE 538 AA; 59800 MW; 1FF33FOAA52B97E4 CRC64;
 CC
 CC Query Match 59.5%; Score 1249; DB 1; Length 538;
 CC Best Local Similarity 63.7%; Pred. No. 3.1e-76;
 CC Matches 247; Conservative 55; Mismatches 64; Indels 22; Gaps 6;
 CC
 CC QY 2 AAPDLLDPKSA--AQNKKRLSFSYKPTVLASRVESDT---TINVMKKTWTSTFLVVL 56
 CC DB 23 AAPVCQPKSATNGHHVPVRLSSIRATVVA-RMEGASQGLQTVNKKTKVVAIFVWV 81
 CC
 CC QY 57 YLIIGATVPKALEQPEHSISORTTIVIQOTFISQHSVCNSTDLELIQIVAAINAGIIP 116
 CC DB 82 YLVTVGLVFRALQEPSSQKNTALEKAEFLRDHICVSPQELTLQHALDADNAGVSP 141
 CC
 CC QY 117 LGNTNQISHWDLGSPFPAGVTITIGRGNISPRTEGKIFCIYALLGIPLFGFLLAG 176
 CC DB 142 VGNSSNSSHWDLGSAFFPAGVTITIGYGNIAAPSTEGKIFCIYAIPLFGFLLAG 201
 CC
 CC QY 177 VGDOLGTIFGKIADVETFIKWNYSOTKIRIISITIFILFGCVLVALPAIFKHIEGW 236
 CC DB 202 IGDQLGTIFGKSIARVEKVRKQVSQTKIRIVISITILFILAGCIVFVTPVAVIKYIEGW 261
 CC
 CC QY 237 SALDAIFYFVITLTITIGFDYVAGG-SDIEYLDYFKPVVWFVILVGLYFAAFLVSMIGDW 295
 CC DB 262 TALESIYFVVTITVGFDFVAGGNAGINREWKPLWFVILVGLYFAAFLVSMIGDW 321
 CC
 CC QY 296 LRVISKKTKEEVEFRAHAAEWANTVAEFKTRRLSVEIYDKPQATSIKRLKSAELIA 355
 CC DB 322 LRVLSKKTKEEVEIKAHAAEWANTVAEFKTRRLSVEIYDKPQATSIKRLKSAELIA 376
 CC
 CC QY 356 GNNHQLTFCRRLTSVNHLTNEDVLP 383
 CC DB 377 -----RRRLGLDQRAHSLDMLSP 394
 CC
 CC RESULT 11
 CC ID CIWA HUMAN STANDARD; PRT; 538 AA.
 CC AC P57789; Q8TDK7; Q8HBS9;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Potassium channel subfamily K member 10 (Outward rectifying potassium
 DE channel protein TREK-2) (TREK-2 K+ channel subunit).
 GN Name=KCNK10; Synonyms=TREK2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORM A).
 RX MEDLINE=20435789; PubMed=1080510; DOI=10.1074/jbc.M002822200;
 RA Lesage F., Terrenoire C., Romey G., Lazdunski M.;
 RT "Human TREK2, a 2p domain mechano-sensitive K+ channel with multiple
 RT regulations by polyunsaturated fatty acids, lysophospholipids and Gs,
 RT Gi, and Gq protein-coupled receptors."; *fed date*
 RL J. Biol. Chem. 275:28398-28405(2000).
 RN [2]
 RN SEQUENCE FROM N.A. (ISOFORMS B AND C).
 RX MEDLINE=21896087; PubMed=11897838;
 RA Gu W., Schlichter G., Hirsch J.R., Engels H., Karschin C.,
 RA Karschin A., Derst C., Steinlein O.K., Daut J.;
 RT "Expression pattern and functional characteristics of two novel splice
 RT variants of the two-pore-domain potassium channel TREK-2."; *fed date*
 RL J. Physiol. (Lond.) 539:657-668(2002).
 CC -!- FUNCTION: Outward rectifying potassium channel. Produces rapidly
 CC activating and non-inactivating outward rectifier K(+) currents.
 CC Activated by arachidonic acid and other naturally occurring
 CC unsaturated free fatty acids.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS;
 CC Name=A; Synonyms=TREK-2a;
 CC IsoId=P57789-1; Sequence=Displayed;
 CC Name=B; Synonyms=TREK-2b;
 CC IsoId=P57789-2; Sequence=VSP_006697;
 CC Name=C; Synonyms=TREK-2c;
 CC IsoId=P57789-3; Sequence=VSP_006698;
 CC -!- TISSUE SPECIFICITY: Abundantly expressed in pancreas and kidney
 CC and to a lower level in brain, testis, colon, and small intestine.
 CC Isoform b is strongly expressed in kidney (primarily in the
 CC proximal tubule) and pancreas, whereas isoform c is abundantly
 CC expressed in brain.
 CC -!- SIMILARITY: Belongs to the two pore domain potassium channel
 CC (TC 1.A.1.8) family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; AF279890; AAG15191.1; -;
 CC EMBL; AF385399; AAL95705.1; -;
 CC EMBL; AF385400; AAL95706.1; -;
 CC Genew; HGNC:6273; KCNK10.
 CC MIM; 605873; -;
 CC GO; GO:0005267; F:potassium channel activity; TAS.
 CC GO; GO:0006810; P:transport; TAS.
 CC InterPro; IPR003280; K+channel_2pore.
 CC InterPro; IPR001622; K+channel_pore.
 CC InterPro; IPR003976; Trek_channel.
 CC PRINTS; PR01333; 2POREKCHANEL.
 CC PRINTS; PR01499; TREKCHANEL.
 CC Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
 CC Potassium; Potassium channel; Transmembrane; Transport;
 CC Voltage-gated channel.
 CC DOMAIN 1 71 Cytoplasmic (Potential).
 CC TRANSMEM 72 92 Potential.
 CC DOMAIN 154 180 Pore-forming 1 (Potential).
 CC TRANSMEM 182 202 Potential.
 CC DOMAIN 203 233 Cytoplasmic (Potential).
 CC TRANSMEM 234 254 Potential.

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FT DOMAIN 263 294 Pore-forming 2 (Potential).
FT TRANSMEM 299 319 Potential.
FT DOMAIN 320 538 Cytoplasmic (Potential).
FT CARBOHYD 144 147 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 147 147 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 1 12 MFPLYDFFLSL -> MKGDRTEGCKRSDS (in isoform B).
FT FTID=VSP 006697.
FT VARSPLIC 1 12 MFPLYDFFLSL -> MKFPIETPRKQVNWDPK (in isoform C).
FT FTID=VSP 006698.
FT CONFLICT 529 529 E -> G (in Ref. 2).
FT SEQUENCE 538 AA; 59764 MW; 8EA615B08D147FBC CRC64;

Query Match 59.2%; Score 1243; DB 1; Length 538;
Best Local Similarity 62.7%; Pred. No. 7.9e-76;
Matches 247; Conservative 54; Mismatches 65; Indels 28; Gaps 6;

QY 2 AAPDLLDPKSA-----AQNKKPLSPSTKPTVLASRVESDT---TINVMKWKTVSTI 50
Db 17 AAAPVCQPKSATNGOPPAPAPTPTPLRSISSRATVVA-RMEGTSQGLQTVMKWKTVAI 75
QY 51 FLAVVYLIIGATVPKALEQPEHISQRTTIVIQKTFISQHSVCVNSTELDELIQIVAAI 110
Db 76 FVWVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLDRHVCVSPQLETLIQHALDAD 135
QY 111 NAGIIPLGNTSNQISHWDLGSGFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPLF 170
Db 136 NAGVSPIGNSSNNSSHWDLSGSAFFAGTIVTTIGYGNIAAPSTEGGKIFCILYVAFGIPLF 195
QY 171 GFLLAGVGDLQGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFPALPAIF 230
Db 196 GFLLAGIGDQLGTIFGKSIARVEKVRKQVSTQKIRVISTITILFLLAGCIVFVTPPAVIF 255
QY 231 KHIEGWSALDAIFYVVTITLTIGFDYVAGG-SDIEYLDYKPVVWFWLVLGLAYFAAVL 289
Db 256 KYIEGWTALIESIFYVVTITLTIGFDGVAGGNAGINREWYKPLVWFWLVLGLAYFAAVL 315
QY 290 SMIGDLRVLSKTKKEEVEGEFRAHAAEWNTANTAEFKETRRRLSVEIYDKFORATSIKRK 349
Db 316 SMIGDLRVLSKTKKEEVEGEIKAHAAEWKANTAEFRETRRLSVEIHDKQRAATIR-- 373
QY 350 LSAELAGNHNQBLTPCRRTLTSVNHJLTNERDVLPP 383
Db 374 -SME-----RRRLGDLQRAHSLDMLSP 394

RESULT 12
Q6B014 PRELIMINARY; PRT; 543 AA.
AC Q6B014;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Potassium channel, subfamily K, member 10, isoform 3.
GN Name=KCNK10;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled tissue;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max3S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pooled tissue;
RA Director MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075022; AAH75022.1; -
DR EMBL; BC075021; AAH75021.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR InterPro; IPR003280; K+channel_2pore.
DR InterPro; IPR001622; K+channel_pore.
DR InterPro; IPR011255; N1r Siralpha_1/3.
DR PRINTS; PR01333; 2PORECHANNEL.
DR PRINTS; PR01499; TREKCHANNEL.
DR Ionic channel.
KW IONIC CHANNEL.
SQ SEQUENCE 543 AA; 60110 MW; 17DB1AFAPAB07C46 CRC64;

Query Match 59.2%; Score 1243; DB 2; Length 543;
Best Local Similarity 62.7%; Pred. No. 7.9e-76;
Matches 247; Conservative 54; Mismatches 65; Indels 28; Gaps 6;

QY 2 AAPDLLDPKSA-----AQNKKPLSPSTKPTVLASRVESDT---TINVMKWKTVSTI 50
Db 22 AAAPVCQPKSATNGOPPAPAPTPTPLRSISSRATVVA-RMEGTSQGLQTVMKWKTVAI 80
QY 51 FLAVVYLIIGATVPKALEQPEHISQRTTIVIQKTFISQHSVCVNSTELDELIQIVAAI 110
Db 81 FVWVVYLVGTGLVFRALQEPFESSQKNTIALEKAEFLDRHVCVSPQLETLIQHALDAD 140
QY 111 NAGIIPLGNTSNQISHWDLGSGFFAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPLF 170
Db 141 NAGVSPIGNSSNNSSHWDLSGSAFFAGTIVTTIGYGNIAAPSTEGGKIFCILYVAFGIPLF 200
QY 171 GFLLAGVGDLQGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFPALPAIF 230
Db 201 GFLLAGIGDQLGTIFGKSIARVEKVRKQVSTQKIRVISTITILFLLAGCIVFVTPPAVIF 260
QY 231 KHIEGWSALDAIFYVVTITLTIGFDYVAGG-SDIEYLDYKPVVWFWLVLGLAYFAAVL 289
Db 261 KYIEGWTALIESIFYVVTITLTIGFDGVAGGNAGINREWYKPLVWFWLVLGLAYFAAVL 320
QY 290 SMIGDLRVLSKTKKEEVEGEFRAHAAEWNTANTAEFKETRRRLSVEIYDKFORATSIKRK 349
Db 321 SMIGDLRVLSKTKKEEVEGEIKAHAAEWKANTAEFRETRRLSVEIHDKQRAATIR-- 378
QY 350 LSAELAGNHNQBLTPCRRTLTSVNHJLTNERDVLPP 383
Db 379 -SME-----RRRLGDLQRAHSLDMLSP 399

RESULT 13
Q68EY1 PRELIMINARY; PRT; 546 AA.
AC Q68EY1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE LOC46288 protein (Fragment).

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CC      IsoId=Q9NYG8-1; Sequence=Displayed;
CC      Name=2; Synonyms=KT4.1b;
CC      IsoId=Q9NYG8-2; Sequence=VSP_006689;
CC      Notes=May be produced at very low levels due to a premature stop
CC      codon in the mRNA, leading to nonsense-mediated mRNA decay;
CC      -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC      (TC 1.A.1.8) family.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; AF248242; AAG31731.1; -
CC      EMBL; AF247042; AAF64062.1; ALT_INIT.
CC      EMBL; AF259500; AAK49389.1; -
CC      EMBL; AF259501; AAK49390.1; -
CC      Genew; HGNC:6279; KCNK4.
CC      MIM; 605720; -
CC      GO; GO:005267; F.potassium channel activity; TAS.
CC      GO; GO:0006813; P.potassium ion transport; TAS.
CC      InterPro; IPR003280; K+channel_2pore.
CC      InterPro; IPR001622; K+channel_pore.
CC      PRINTS; PR01333; 2POREKCHANNEL.
CC      PRINTS; PR01691; TRAAKCHANNEL.
CC      Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW      Potassium; Potassium channel; Transmembrane; Transport;
KW      Voltage-gated channel.
FT      DOMAIN 1 3 Cytoplasmic (Potential).
FT      TRANSMEM 4 24 Potential.
FT      DOMAIN 89 113 Pore-forming 1 (Potential).
FT      TRANSMEM 118 138 Potential.
FT      DOMAIN 139 171 Cytoplasmic (Potential).
FT      TRANSMEM 172 192 Potential.
FT      DOMAIN 197 221 Pore-forming 2 (Potential).
FT      TRANSMEM 234 254 Potential.
FT      DOMAIN 255 393 Cytoplasmic (Potential).
FT      CARBOHYD 78 78 N-linked (GlcNAc...) (Potential).
FT      CARBOHYD 82 82 N-linked (GlcNAc...) (Potential).
FT      VARSPLIC 1 1 M -> MTTAQEPAPRPLQAGSGAGPAPGRAM (in
FT      isoform 2).
FT      /FTId=VSP_006689.
FT      P -> L (in Ref. 2).
FT      CONFLICT 328 328 P -> L (in Ref. 2).
FT      SEQUENCE 393 AA; 42704 MW; 7F18E53A0A9AD57D CRC64;
SQ
Query Match 38.2%; Score 803; DB 1; Length 393;
Best Local Similarity 51.1%; Pred. No. 3e-46;
Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
QY 42 MKWKTSTIFLVVLYLTIGATVFKALEQHPFISQRTTIVQKTFISQHSVNSTELDE 101
Db 1 MRSTTLALLLVLLVSGALVFRALEQHPFISQRTTIVQKTFISQHSVNSTELDE 60
QY 102 LQQIIVAAINAGIIPGNTSNQISH--WDLGSSFFPAGTIVITIGFNSIPRTEGKIFC 159
Db 61 LIKEVADALGGGADPNTNSTSSHSADWLGSAFFSGTITITIGYGNVALRTDAGRLFC 120
QY 160 IYVALLGIPFLGGLLAGVGDLGTIFGKIAKVEDTFIKWVYSQTKIRIISTIFLFGC 219
Db 121 IFVALVGIPLFGLLAGVGDLGSSLRHGIGHEALFLKWHVPPELVRVLSMLFLIGC 180
QY 220 VLFVALPAIFKHIEGWSALDAIFYVITLITIGFGDYVAGGSDIEYLFYKPVVWFIL 279
Db 181 LLFVLTPTFVFCVWEDWSKLEALFYFVITLITIGFGDYVAGGSDIEYLFYKPVVWFIL 240
QY 280 VGLAYPAVLSMIGDWLNRVLSKTKKEVEGFRAHAAEWANTVA 323
Db 241 LGLAYPASVLTITGNLVRVSRTRAEWGGLTAQAASWTGTVA 284
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RESULT 15
CIW4 MOUSE
ID CIW4 MOUSE STANDARD; PRT; 398 AA.
AC O88454;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Potassium channel subfamily K member 4 (TWIK-related arachidonic acid-
DE stimulated potassium channel protein) (TRAAK).
GN Name=Kcnk4; Synonyms=TRAAK;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98292450; PubMed=9628867; DOI=10.1093/emboj/17.12.3297;
RA Fink M., Lesage F., Duprat F., Heurteaux C., Reyes R., Fosset M.,
RA Lazdunski M.;
RT "A neuronal two P domain K+ channel stimulated by arachidonic acid and
RT polyunsaturated fatty acids.";
RL EMBO J. 17:3297-3308(1998).
RN [2]
RP ACTIVATION.
RX MEDLINE=99254548; PubMed=10321245; DOI=10.1038/8084;
RA Patel A.J., Honore E., Lesage F., Fink M., Romey G., Lazdunski M.;
RT "Inhalational anesthetics activate two-pore-domain background K+
RT channels.";
RL Nat. Neurosci. 2:422-426(1999).
CC -1- FUNCTION: Voltage insensitive, instantaneous, outwardly rectifying
CC potassium channel. Outward rectification is reversed at high
CC external K(+) concentrations.
CC -1- SUBUNIT: Homodimer (Potential).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O88454-1; Sequence=Displayed;
CC Name=2; Synonyms=TRAAK; Truncated;
CC IsoId=O88454-2; Sequence=VSP_006690, VSP_006691;
CC -1- TISSUE SPECIFICITY: Expressed in brain, spinal cord and eye. Not
CC detected in heart, skeletal muscle, liver, lungs, kidney and
CC testis.
CC -1- MISCELLANEOUS: Activated by arachidonic acid and other unsaturated
CC fatty acids. Not affected by volatile general anaesthetics such as
CC chloroform, diethyl ether, halothane and isoflurane.
CC -1- SIMILARITY: Belongs to the two pore domain potassium channel
CC (TC 1.A.1.8) family.
CC
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC
CC      EMBL; AF056492; AAC40181.1; -
CC      MGD; MGI:1298234; Kcnk4.
CC      InterPro; IPR003280; K+channel_2pore.
CC      InterPro; IPR001622; K+channel_pore.
CC      InterPro; IPR008074; TRAAK_channel.
CC      PRINTS; PR01333; 2POREKCHANNEL.
CC      PRINTS; PR01691; TRAAKCHANNEL.
CC      Alternative splicing; Glycoprotein; Ion transport; Ionic channel;
KW      Potassium; Potassium channel; Transmembrane; Transport;
KW      Voltage-gated channel.
FT      DOMAIN 1 3 Cytoplasmic (Potential).
FT      TRANSMEM 4 24 Potential.
FT      DOMAIN 89 113 Pore-forming 1 (Potential).
FT      TRANSMEM 119 139 Potential.
```

FT DOMAIN 140 171 Cytoplasmic (Potential).
FT TRANSMEM 172 192 Potential.
FT DOMAIN 198 222 Pore-forming 2 (Potential).
FT TRANSMEM 235 255 Potential.
FT DOMAIN 256 398 Cytoplasmic (Potential).
FT CARBOHYD 81 81 N-linked (GlcNAc. .) (Potential).
FT CARBOHYD 84 84 N-linked (GlcNAc. .) (Potential).
FT VARSPLIC 63 67 KILVE -> KAMAI (in isoform 2).
FT VARSPLIC 68 398 /FTid=VSP_006690.
FT VARSPLIC 68 398 Missing (in isoform 2).
FT /FTid=VSP_006691.
SQ SEQUENCE 398 AA; 43051 MW; 478A834B7B7AEC92 CRC64;
Query Match 37.0%; Score 776.5; DB 1; Length 398;
Best Local Similarity 49.8%; Pred. No. 1.9e-44;
Matches 142; Conservative 57; Mismatches 83; Indels 3; Gaps 1;
QY 42 MKWKTIVSTIFLVVLYLIIGATVFKALQPHQHEISQRTTIVIQKQTFISQHSQVNSTELDE 101
Db 1 MRSITLLALLVLYLVSGALVQALQPHQHEQQAQKQMDHGRDQFLRDHPCVSKSLED 60
QY 102 LIQIIVAINAGIIP---LGNISNOISHWDLGSSFFAGTVITTTIGFQGNISPRTEGGKIF 158
Db 61 FIKLVEALGGGANPETSWTNSNHNSSAWNLGSAFFSGTITTTIGYGNIVLHTDAGRLF 120
QY 159 CIIYALGIGPLGFLAGVGDLGTIFGKGIKVEDTFIKWVSOVKIRIISTIFIILFG 218
Db 121 CIFYALVGIPLFGMLAGVGRGLGSSLRGGHIEAIFLKHVPPCLVRSLSAVLFLIG 180
QY 219 CVLFVALPAIIPKHIEGWSALDAIYFVVITLTITGFDYVAGGSDIEYLDYKPVVWFMI 278
Db 181 CLLFVLTPTFFVSYNESKLEAIYFVIVTLTTVVGFDYVPGDGTGQNSPAYQPLVWFMI 240
QY 279 LVGLAYFAVLGMIGDNLRLVISKTKYEEVGEFRAHAETANVTA 323
Db 241 LFGLAYFASVLTITIGNWLRVSRRTAEMGGLTAQASWGTGTVA 285

Search completed: July 13, 2005, 08:44:29
Job time : 96.9622 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:02:40 ; Search time 21.6316 Seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-09-503-089a-2
Perfect score: 2100
Sequence: 1 MAAPDLLDPKSAQNSKPL.....LNGLTPHCAGEIAVNIK 411
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	379.5	18.1	336	2 S65566	inward rectifier p
2	347.5	16.5	330	2 JC7703	TASK-5 protein - h
3	345	16.4	329	2 T43509	probable potassium
4	331.5	15.8	336	2 T32347	outward rectifier
5	319	15.2	1001	2 T13807	potassium channel
6	288	13.7	383	2 T23182	hypothetical prote
7	284.5	13.5	334	2 T19860	hypothetical prote
8	284.5	13.5	364	2 T43361	probable potassium
9	282.5	13.5	461	2 T43394	potassium channel
10	279	13.3	393	2 T23392	hypothetical prote
11	273	13.0	392	2 T45032	hypothetical prote
12	273	13.0	1910	2 H88124	protein T12C9.3 (i
13	269	12.8	325	2 T15584	hypothetical prote
14	266	12.7	522	2 T24265	hypothetical prote
15	262	12.5	452	2 T21118	hypothetical prote
16	249.5	11.9	427	2 T27681	hypothetical prote
17	247	11.8	444	2 T26229	hypothetical prote
18	245.5	11.7	1539	2 T30037	hypothetical prote
19	244.5	11.6	513	2 T28933	hypothetical prote
20	240	11.4	524	2 T23907	hypothetical prote
21	236.5	11.3	528	2 T21834	hypothetical prote
22	236	11.2	643	2 T26616	hypothetical prote
23	230	11.0	443	2 T21598	hypothetical prote
24	228.5	10.9	484	2 T43529	probable potassium
25	228.5	10.9	519	2 T16629	hypothetical prote
26	227	10.8	550	2 T22557	hypothetical prote
27	224	10.7	1136	2 T28953	hypothetical prote
28	218	10.4	307	2 H89074	protein twk-24 (lm
29	218	10.4	485	2 T24201	hypothetical prote

30	217.5	10.4	335	2 S44635	f22b7.7 protein -
31	217.5	10.4	544	2 T43364	potassium channel
32	217.5	10.4	551	2 T16426	hypothetical prote
33	217.5	10.4	555	2 T43357	potassium channel
34	217.5	10.4	576	2 T43363	potassium channel
35	217.5	10.4	691	2 S45585	outward-rectifier
36	217	10.3	475	2 T27725	hypothetical prote
37	215.5	10.3	586	2 T21683	hypothetical prote
38	211	10.0	660	2 T21551	hypothetical prote
39	205.5	9.8	381	2 T43393	potassium channel
40	205.5	9.8	769	2 T27550	hypothetical prote
41	205	9.8	700	2 T27364	hypothetical prote
42	204.5	9.7	523	2 T23373	hypothetical prote
43	202.5	9.6	539	2 T23700	hypothetical prote
44	196	9.3	681	2 T19429	hypothetical prote
45	195.5	9.3	569	2 T43531	probable potassium

ALIGNMENTS

RESULT 1

S65566
inward rectifier potassium channel TWIK-1 - human
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S65566
R:Lesage, F.; Guillemare, E.; Fink, M.; Duprat, F.; Lazdunski, M.; Romey, G.; Barhanin, E.MBO J. 15, 1004-1011, 1996
A:Title: TWIK-1, a ubiquitous human weakly inward rectifying K(+) channel with a novel
A:Reference number: S65566; MUID:96183184; PMID:8605869
A:Accession: S65566
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-336 <LES>
A:Cross-references: UNIPROT:O00180; EMBL:U33632; NID:g1086490; PIDN:AA801688.1; PID:g10

Query Match 18.1%; Score 379.5; DB 2; Length 336;
Best Local Similarity 32.5%; Pred. No. 3.5e-23;
Matches 90; Conservative 62; Mismatches 108; Indels 17; Gaps 9;

QY	51	FLVW--VLYLIIGATVFKALEOPHEISQRTTIVIOKQFISQHSVCNSTELDELIIQIIVA	108
DB	25	FLVLYLLYLVFGAVVFSVELPFDLLRQELKRLKRRFLEHECLSEQQLQFLGRVLE	84
QY	109	AINAGHIPLGNTSNQISHWDLGSSFFFACTVTTTIGFNGISPRTEGGKIFCIYALLGIP	168
DB	85	ASNYGVSVLSNASGN-WNWDFTSALFFASTVLTSTGYGHTVPLSDGGKAFCIYVIGIP	143
QY	169	LFGPILLAGVGDQLGTIFKGIKAKVEDTFIKNVVSTKIRIISTII--FILFGCVLFPALP	226
DB	144	FTLLFLTAVVQRITVHVTR--RPVLYFHIRMGFSKQVVAIVHAVLILGFVTVSCFFPI--P	199
QY	227	AIIPKHIE-GWSALDAIYFVITLTIGFGDVVAG-GSDIEVLDYFKPVVWFILGLAY	284
DB	200	AAVFSVLEDDWNFLSEFYFCFISLTIGLDYVPGEGYNQKPRELYKIGITCYLLGLIA	259
QY	285	PAAVLSMIGDMLRVISK-----KTKEEVEGFRAHAAE	316
DB	260	MLVLETTCF-LHEKKFKRMFYVKDKDDQVHLIE	295

RESULT 2

JC7703
TASK-5 protein - human
C:Species: Homo sapiens (man)
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: JC7703
R:Kim, D.; Gnatenco, C.
Biochem. Biophys. Res. Commun. 284, 923-930, 2001
A:Title: TASK-5, a new member of the tandem-pore K+ channel family.
A:Reference number: JC7703; MUID:21303050; PMID:11409881
A:Accession: JC7703


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Query Match      15.2%; Score 319; DB 2; Length 1001;
Best Local Similarity 28.4%; Pred. No. 1.1e-17;
Matches 89; Conservative 61; Mismatches 127; Indels 36; Gaps 10;

QY 50 IFLVVLYLIIGATVFKALEQPH-----ISQRTIVIQKQFFISQHSVCVNSTELDELIQ 105
DB 9 LLIFYLYLMFGAIIYHIEHBKESRAEQKQAIAINEYLLEELGDKNTTQDEILQR 68

QY 106 IVAAINAGIPLGNTSQISHWDLGSGFFAGVTTTIGFNGISPRTEGKIFCIYALL 165
DB 69 ISDYCDKPVLTPTDYDDPTWTFYHAFFAFTVCSIVGYNISPTTFAGRMIMIAYSVI 128

QY 166 GIPFLGFLAGVDQGLTIFGKIAKVEDTFIKNNVS-----QTKIRIISTIFIILF-G 218
DB 129 GIPVNGILFAG-----LCEYEGRTFEAIYRYKYNKSTDMHYPPQGLITTVVIALIP 184

QY 219 CVLFPVALPAIIEKHIEGMSALDAIYFVWITLTITIGGDYVA-----GSGDIEYLD 268
DB 185 IALFLLPLSVWFTYFENWPNYSISLYSYVTTTIGFGDYVPTTFGANQPKFEGGFWVYQI 244

QY 269 FYKPVVFWFLVGLAYFAAIVLSMIGDMLRVISKK---TKEEVGEFRAHAHAETANVTAE 324
DB 245 FV--IWF--IFSLGVLVMTITRGLQ--SKLAYLEQQLSSNLKATQNRIMWSGVTKD 298

QY 325 FKETRRRLSVEIY 337
DB 299 VGYLRRLN-ELY 310

RESULT 6
T23182
hypotheical protein K01D12.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23182
R:Dobson, R.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19703
A:Accession: T23182
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-383 <WIL>
A:Cross-references: UNIPROT:Q21094; EMBL:Z75543; PIDN:CAA99871.1; GSPDB:GN00023; CESP:K01D12.4
A:Experimental source: clone K01D12
C:Genetics:
A:Gene: CESP:K01D12.4
A:Map position: 5
A:Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

Query Match      13.7%; Score 288; DB 2; Length 383;
Best Local Similarity 23.6%; Pred. No. 1.1e-15;
Matches 85; Conservative 80; Mismatches 127; Indels 68; Gaps 12;

QY 20 LPSSTKPTVLASVESDTTINNMKKT-VSTIFLVVLYLIIGATVFKALEQPHISQRT 78
DB 16 LRANTLPSITRAKVGCGFARLRYEENARFVLCIILIVYLAFAAILFHWLEWENYDERI 75

QY 79 TI---VIOKQTFISQHSVCVNSTELDELIQIVAAINAGIPLGNTSQISHWDLGSGFF 135
DB 76 AIDNRWADYQVKYCKRKLNECFEENVRPISDQATSGLL-----NSRSPDHLGSLFF 129

QY 136 AGTVTTTIGFNGISPRTEGKIFCIYALIG-----IPLFGFLAGVDQGLTIFGKIAK 191
DB 130 SATVISTIGTSTPRTHLGRFTITVYGVGCTCCVLFPNLF-----ERLVGMSYILAS 185

QY 192 VEDTFIKNNVSQTKIRIISTII-----FILFG-CVLFFV 223
DB 186 LRERKIRYRLKSGKNPVTLLLNEDFNESSSCGGHMDNWRPSVYKVPFILFPMCLVLI 245

QY 224 ALPAIIFKHIEGMSALDAIYFVWITLTITIGFGDYVAGSDIEYL--DFYKPVVFWILV 281
DB 246 TASAGIYSVVENWNYIDSLYFCFISPATIGFGDYVSNQDQVTRMSPDLYRFVNFCLLTIG 305

Query Match      15.2%; Score 319; DB 2; Length 1001;
Best Local Similarity 28.4%; Pred. No. 1.1e-17;
Matches 89; Conservative 61; Mismatches 127; Indels 36; Gaps 10;

QY 50 IFLVVLYLIIGATVFKALEQPH-----ISQRTIVIQKQFFISQHSVCVNSTELDELIQ 105
DB 9 LLIFYLYLMFGAIIYHIEHBKESRAEQKQAIAINEYLLEELGDKNTTQDEILQR 68

QY 106 IVAAINAGIPLGNTSQISHWDLGSGFFAGVTTTIGFNGISPRTEGKIFCIYALL 165
DB 69 ISDYCDKPVLTPTDYDDPTWTFYHAFFAFTVCSIVGYNISPTTFAGRMIMIAYSVI 128

QY 166 GIPFLGFLAGVDQGLTIFGKIAKVEDTFIKNNVS-----QTKIRIISTIFIILF-G 218
DB 129 GIPVNGILFAG-----LCEYEGRTFEAIYRYKYNKSTDMHYPPQGLITTVVIALIP 184

QY 219 CVLFPVALPAIIEKHIEGMSALDAIYFVWITLTITIGGDYVA-----GSGDIEYLD 268
DB 185 IALFLLPLSVWFTYFENWPNYSISLYSYVTTTIGFGDYVPTTFGANQPKFEGGFWVYQI 244

QY 269 FYKPVVFWFLVGLAYFAAIVLSMIGDMLRVISKK---TKEEVGEFRAHAHAETANVTAE 324
DB 245 FV--IWF--IFSLGVLVMTITRGLQ--SKLAYLEQQLSSNLKATQNRIMWSGVTKD 298

QY 325 FKETRRRLSVEIY 337
DB 299 VGYLRRLN-ELY 310

RESULT 6
T23182
hypotheical protein K01D12.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23182
R:Dobson, R.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z19703
A:Accession: T23182
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-383 <WIL>
A:Cross-references: UNIPROT:Q21094; EMBL:Z75543; PIDN:CAA99871.1; GSPDB:GN00023; CESP:K01D12.4
A:Experimental source: clone K01D12
C:Genetics:
A:Gene: CESP:K01D12.4
A:Map position: 5
A:Introns: 28/3; 76/3; 184/2; 217/2; 270/2; 295/2

Query Match      13.7%; Score 288; DB 2; Length 383;
Best Local Similarity 23.6%; Pred. No. 1.1e-15;
Matches 85; Conservative 80; Mismatches 127; Indels 68; Gaps 12;

QY 20 LPSSTKPTVLASVESDTTINNMKKT-VSTIFLVVLYLIIGATVFKALEQPHISQRT 78
DB 16 LRANTLPSITRAKVGCGFARLRYEENARFVLCIILIVYLAFAAILFHWLEWENYDERI 75

QY 79 TI---VIOKQTFISQHSVCVNSTELDELIQIVAAINAGIPLGNTSQISHWDLGSGFF 135
DB 76 AIDNRWADYQVKYCKRKLNECFEENVRPISDQATSGLL-----NSRSPDHLGSLFF 129

QY 136 AGTVTTTIGFNGISPRTEGKIFCIYALIG-----IPLFGFLAGVDQGLTIFGKIAK 191
DB 130 SATVISTIGTSTPRTHLGRFTITVYGVGCTCCVLFPNLF-----ERLVGMSYILAS 185

QY 192 VEDTFIKNNVSQTKIRIISTII-----FILFG-CVLFFV 223
DB 186 LRERKIRYRLKSGKNPVTLLLNEDFNESSSCGGHMDNWRPSVYKVPFILFPMCLVLI 245

QY 224 ALPAIIFKHIEGMSALDAIYFVWITLTITIGFGDYVAGSDIEYL--DFYKPVVFWILV 281
DB 246 TASAGIYSVVENWNYIDSLYFCFISPATIGFGDYVSNQDQVTRMSPDLYRFVNFCLLTIG 305

Query Match      13.5%; Score 284.5; DB 2; Length 364;
Best Local Similarity 27.4%; Pred. No. 2e-15;

QY 282 LAYF-----AAVLSMIGDMLRVISKTKEEVGEFRAHAHAETANVTAEFKETRRRLSV 334
DB 306 ACFFYCLSVSSIVVRQLLNWM---IKMDVKV-EDRSPFLC-----FKKRRYMG 352

RESULT 7
T19860
hypotheical protein C40C9.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19860
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19860
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-334 <WIL>
A:Cross-references: EMBL:Z70266; PIDN:CAA94204.1; GSPDB:GN00028; CESP:C40C9.1
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.1
A:Map position: X
A:Introns: 34/1; 60/2; 98/1; 145/3; 160/3; 181/1; 204/1; 252/2; 279/2; 306/3

Query Match      13.5%; Score 284.5; DB 2; Length 334;
Best Local Similarity 27.4%; Pred. No. 1.8e-15;
Matches 86; Conservative 63; Mismatches 112; Indels 53; Gaps 11;

QY 50 IFLVVLYLIIGATVFKALEQPHISQRTIV---IQKQTFISQHSVCVNSTELDELIQ 106
DB 14 LILSTFTYLLFGAMVFDKLE-----SEKDTWVRDEITERITDRLKHK-YNFSERDLHLFEA 67

QY 107 VAAINAGIPLGNTSQISH-WDLGSGFFAGVTTTIGFNGISPRTEGKIFCIYALL 165
DB 68 IA-----IKSIPOQAGYQMFAGATVTTITVGYGHSAPSTNAGKLCFMIFALP 119

QY 166 GIPFLGFLAGVDQGLTIFGKIAKVEDTFIK-----WNVSQTKIRIIS-TIIFILFG 218
DB 120 GVPMLIMFQSIGERVNTFIAYSLHKFRDSLHQOQFTCLQEVTPTHLLMVSLTIGFVW-- 177

QY 219 CVLFPVALPAIIEKHIEGMSALDAIYFVWITLTITIGFGDYV--AGGSDIEYLDYKPVVWF 276
DB 178 ----IVSGTYMFHTIEKNSIFDAYFYFCMITFTSTIGFDLVPLQQVNALQDQPLYVFATIM 233

QY 277 WILVGLAYFAAIVLSMIGDMLRVISKTKEEVGEFRAHAHAETANVTAEFKETRRRLSVEI 336
DB 234 FIIIGLAVFSACVNL-----VLGFMASNADEVTA-----AQREPPSAIV 273

QY 337 YDKFORATSIKRKL 350
DB 274 LERFTNSLVDSQI 287

RESULT 8
T43361
probable potassium channel chain n2p20 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43361
R:Wang, Z.W.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in C. elegans.
A:Reference number: Z22450
A:Accession: T43361
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-364 <WAN>
A:Cross-references: UNIPROT:O76790; EMBL:AF083646; PIDN:AAC32857.1

Query Match      13.5%; Score 284.5; DB 2; Length 364;
Best Local Similarity 27.4%; Pred. No. 2e-15;
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Matches	86;	Conservative	63;	Mismatches	112;	Indels	53;	Gaps	117
Qy	50	IFLVVLYLIIGAVFKALEOPHEISORTTIV---	IOKQTEISOHSCVNSTELDELQIQI	106					
Db	14	LILSTFYLLFGANVFKLE-----	SEKQTVWRDEIERITDRLXHK-YNFSERDLHLPEA	67					
Qy	107	VAAINAGIILPLGNTSNQISH-WDLGSGFFFA	GVTTVITTFIGNISPRTEGKIFCIIVALL	165					
Db	68	IA-----	IKSPIQQAGYQWQFAGAFYFATVTVITTVGYGHSAPSTNAGKLCFQWIFALF	119					
Qy	166	GIPFLGELLAGVDQLGTIFGKGAKVEDFIK-----	WNVSQTKIRIIS-TIIFILFG	218					
Db	120	GVPMGLIMFOSIGERVNTFIAYSLLHKFRDSL	HHQQGFTCLQEVVTPTHLLMVSLLTIGFMV--	177					
Qy	219	CVLFVVALPAIFKHIEGWSALDAYVYVITLT	TITIGFGDYV--AGGSDIEYLDYFKVPVWF	276					
Db	178	-----	IVSGTYMFHTYETKWSIFDAYFCWITESTTIGFGLVPLQQVNALQDQPLVFATIM	233					
Qy	277	WILVGLYFAVLVSNIGMDLWRVISKTKKEEYGE	FFRAHAAEWANTVNTAEFKETRRRLSVEI	336					
Db	234	FILLGLAVFSACVNL-----	VLGFWASNADEVTA-----AQREPPSAIV	273					
Qy	337	YDKPQRATSIKRKL	350						
Db	274	LERFTRNSLVD	SOI	287					

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RESULT 9
T43394
potassium channel chain n2P18 homolog - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43394
R:Kunkel, M.T.; Salkoff, L.
submitted to the EMBL Data Library, August 1998
A:Description: Potassium channels in C. elegans.
A:Reference number: Z22479
A:Accession: T43394
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-461 <KUN>
A:Cross-references: UNIPROT:Q18120; EMBL:AF083650; PIDN:AAAC32861.1

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[illegible]

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Db      337 VDEEDENNKKSPDAV--ISRMTNWSKRGLYLLPDSQKKELAKQSEKKMGKRSIKIQ-- 399
Qy      375 TNERDVLPLPKTE 388
       :|:|:|:|
Db      393 -TNDLLETIREE 405

RESULT 10
T25392
hypothetical protein T28A8.1 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: T25392
R/Lloyd, C.
submitted to the EMBL Data Library, March 1997
A/Reference number: Z20027
A/Accession: T25392
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: DNA
A/Residues: 1-393 <WTL>
A/Cross-references: UNIPROT:Q9XU07; EMBL:Z92813; PIDN:CAB07286.1; GSPDB:GN0002
A/Experimental source: clone T28A8
C/Genetics:
A/Gene: CESP:T28A8.1
A/Map position: 3
A/Introns: 73/1: 112/3: 179/2: 209/3: 287/2: 310/3: 364/2

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	Query Match	13.3%;	Score 279;	DB 2:	Length 393;	
	Best Local Similarity	27.06;	Pred. No.	6.le-15;		
	Matches 81; Conservative	54;	Mismatches 107;	Indels 58;	Gaps 9	
Qy	44 WKTVSTIFL-----VVVLIIIGATVFKALEOPHEISORTIIV----IQKTFIS--- 89 : : : : : : : : :					
Dd	4 WKTVARIILAHSVLSLVSVVVVGAFLEYOLEQPNEVEVRARNIERFNIHKROMIEHLW 63 : : : : : : : : :					
Qy	90 --QHSCVNSTELDELIQQIVAANINAGIIPGNT-----SNQISHWDLGSSPEFF 135 ::: :::: : : : : : : : :					
Dd	64 EMRESGGTGHVEDLAYKVYVDNVNTRILFEAPDTHCIGAHLRPGGEDEDNNWTYTALPF 123 : : : : : : : : :					
Qy	136 AGTVTITTGFGNISPRTEGGKGIFCIICALLGIPLFGFLLAGVGD-----OLGTIFGKG 188 : : : : : : : : : :					
Dd	124 TTTLTTTIGYNLPVTGRGKLCLCILVALFGVPLLILTVAIDGKFELSEINVQLTYWRXKL 183 : : : : : : : : : :					
Qy	189 IAKVEDTFIKWNVSQTk-----IRISTIFIILFGCVLFVALPALPIFKHI 233 : : : : : : : : : :					
Dd	184 REKCSKO--KYVSFTSKDKRKNGEGLNDJHLENYISIFILFAILLSTYTPFGAVLSLMW 241 : : : : : : : : : :					
Qy	234 EGWSALDAIFYPWWITLTITGFEGDVVAGGSDI EYLD FYPVVMFWTILVGLAYFAA VLSMTG 293 : : : : : : : : : :					
b	242 EGNDFPSGSEFSPTMTTVSGFDIVPKREVVYLDEL-----CYIII GLSITMCMCIDLVG 295 : : : : : : : : : :					

RESULT 11
T45032
hypothetical protein Y39B6.f [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C:Accession: T45032
R:Wilson, R.; Ainscough, R.; Anderson, K.; Baynes, C.; Berks, M.; Bonfield, J.;
raser, A.; Fulton, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier,
B.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders
Nature 368, 32-38, 1994
A:Authors: Wilkenson, R.; Sims, M.; Smaildon, N.; Smith, A.; Smith, M.; Sonnham
tock, L.; Wilkinson-Sproat, J.; Wohlman, P.
A:Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. el
A:Reference number: S43531; MUID:94150718; PMID:7906398
A:Accession: T45032
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-392 <Wtl>
A:Cross-references: NID:G6434440; PIDN:CAB60911.1; PID:G6434446
A:Experimental source: Clone Y39B6
C:Genetics:

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339 TTMATIGVGNIVPTPLGRCLACVLFGALPGAPIAITITIGDLGKFLSECTIWLKYHWRKGS 399
QY 191 KVEDTFIKW-----NVSQTKIRIISTITIFILFGCV 220
Db 399 RLDSAWKFRGLESDISDDLESASKNQSSILDMDEIDKSEVPVLAVFTII-----L 452
QY 221 LFVALPALIFKHIEGWSALDAIYFVVTLLTIGRGDYVAGSDIBYLFDPYKPVVFWILY 280
Db 453 LYIAFGGILFSLIEDWSYMDAFYYSFSLTTIGFGDIVPENHD-----YIAIMLIYLG 506
QY 281 GLAYFAAVLSMIG-----DWLRVISKTK-----EVEGEFRAH 313
Db 507 GLSVTTCIDUAGIQYQKIHFGKFGQGTDLQLYKKRMLERRLANGQGEIILRKVTH 566
QY 314 AAETVANTVTAEFKESTRRLSVEIYDK 339
Db 567 AVE-----KFEREQQLQKMEEE 585

RESULT 13
T15584
hypotheical protein C24A3.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15584
R:Favellio, T.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C24A3.
A:Reference number: Z18373
A:Accession: T15584
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-325 <FAV>
A:Cross-references: EMBL:U40424, NID:g1065542; PID:g1065543; PIDN:AAA81455.1;
C:Genetics:
C:Gene: CESP:C24A3.6
A:Introns: 21/1, 63/3, 131/1, 193/3; 206/3

Query Match 12.8%; Score 269; DB 2; Length 325;
Best Local Similarity 25.1%; Pred. No. 3.1e-14;
Matches 86; Conservative 53; Mismatches 88; Indels 116; Gaps 11

QY 46 TVSTIF-----LVVYLLIGATVFKALQPHISORTTIVIQKTFISQHSVCN 95
Db 10 TILTFQKTPKGLPLIILVAYTLGAWIFWMEIGENE-----REMLIEQK--- 56
QY 96 STELDELIIQIVAIN-----AGIILPGNTSNOIS 125
Db 57 --ERDELIRTVYKINLOIQKRRLMTABEYNRTAKVLTFTQETLGIVPA--DMDKDI 112
QY 126 HWDLGSSFFAGTVITIGFNISPRTEGGKIFGCIIVALLGIPFGFLLAGVGDLGTIF 185
Db 113 HWTFLGSIFCVMTVYTIIGVNIIVPGTGWGRFATILYAFIGIPLTVLSLY----CLGSLF 168
QY 186 GKGIKVEDTFIKWNSQTKIRIS----- 210
Db 169 AKGCKMLWRFFLK-----STRVVSKDLSNKISEADNIEBGTAITPSAEKTENNDDDL 222
QY 211 ---TIIFILFGCVLFVALPALIFKHIEGWSALDAIYFVVTLLTIGRGDYVAGSDIBYL 267
Db 223 LSPFISGLLITVIWVIFCAVLFTLEEDWFGTSLYFTLISFTTIGFGDILP--SDYDFM 280
QY 268 DFYKPVVFWILVGLAYFAAVLSMIGDWRVIS-----KKTKE 305
Db 281 ----PIGVLLILGLSVSTWTLIIQQOIEALSVRRRKKKK 319

RESULT 14
T24265
hypotheical protein T01B4.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T24265

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R;Wilkinson, J.
submitted to the EMBL Data Library, March 1996
A;Reference number: Z19866
A;Accession: T24265
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-522 <W1>
A;Cross-references: UNIPROT:Q22042; EMBL:Z70036; PIDN:CAA93875.1; GSPDB:GN00028; CESP:TQ
A;Experimental source: clone T01B4
C;Genetics:
A;Gene: CESP:T01B4.1
A;Map position: X
A;Introns: 95/3; 142/1; 224/3; 290/1; 458/1

Query Match	12.7%	Score 266;	DB 2;	Length 522;
Best Local Similarity	23.1%	Fred.No.	9.7e-14;	
Matches	99;	Conservative	64;	Mismatches 132; Indels 134; Gaps 15
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Db	41	L I L I I L G Y A C L G G Y M F Q A L E Y D Q Q O L E L E A E K R V L S E S S L L A V N L L E H L K Q M N C G Q S N E		100
Qy	99	L D E L I Q U I V A A I N A G I I P L G N T S - N Q I S H W L D G S F F P A G T V I T T I G C N I S P R T E G K I		157
Db	101	K R C L E I T T K T F I Q R S D E E R G E G R W D F W N S V F E S A T F I T T I G Y L N L A C K T N L G R I		155
Qy	158	F C I I V A L I G I P L F G F L A G V D -----	Q L G T I F G K	188
Db	156	A T I I Y G M I G I P L M L F V L K N F G E L C V K W A K K I Q F N V Q O C L K K C F G R K Q K R A S S L A S I T S K E		215
Qy	189	I A K V -----	E D T P - - I K N V S Q T K I R I S T I T F I L F G C V L F V A L P A I F K H I E G W S	237
Db	216	M L E V F E F V E P D D K E D T T F Q L R W G -----	L L V I L F V L I C S F V S F W E N W D	260
Qy	238	A L D A I Y F V V I L T T I G F G D Y V A G S D I E Y L D F Y K P V V W F I L - - V G L A Y F A A V L S M I G D -		294
Db	261	F L T A Y F F F V S L T I G F G D I V P -----	D H P R T A C A L F V L Y F I G L A L F A M V Y A I L Q E R	312
Qy	295	- - - - - W - L R V I S K K T E E V G E F R A H A A E W T A N V T - - - - -		322
Db	313	V E N Q Y M W A L E I T D Q Y O K L Q D M Y D E D E K K A D N D M H F S K K E P V R G P R I I L Q D L L R G P D		372
Qy	323	A E P K E T R R L S - - - - - V E I Y D K F O R A T S I K K L S A E L - - - - -	A G N H N O E L T P C R R T L S	370
Db	373	L K I S G R R S S D A S S V I T E A S D E D T R H F K V G R A I L A E A F A P D E R A S N H G T Q L N S C T - - - - -		428
Qy	371	V N H L T N E R D		379
Db	429	- - - V S N E H D		434

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RESULT 15
T21118
hypothetical protein F19D8.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T21118
R:Swingburne, J.; Ainscough, R.
submitted to the EMBL Data Library, August 1996
A:Reference number: Z19377
A:Accession: T21118
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-452 <WIL>
A:Cross-references: UNIPROT:Q93531; EMBL:Z78541; PIDN:CAB01740.1; GSPDB:GN00028; CESP:F19D8
A:Experimental source: clone F19D8
C:Genetics:
A:Gene: CESP:F19D8.1
A:Map position: X
A:Introns: 31/1; 82/2; 101/3; 157/1; 197/1; 230/3; 267/2; 325/3; 356/1; 404/3

Query Match      12.5%      Score 262;  DB 2;  Length 452;
Best Local Similarity 28.5%      Pred. No. 1.7e-13;

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 13, 2005, 08:40:02 ; Search time 90.2442 Seconds
(without alignments)
1759.475 Million cell updates/sec

Title: US-09-503-089A-2
Perfect score: 2100
Sequence: 1 MAAPDLLDPKSAQNSKPRL.....LNLTPHCAGEIAVNIK 411

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1726220 seqs, 386332138 residues

Total number of hits satisfying chosen parameters: 1726220

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
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20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2100	100.0	411	11	US-09-892-360-18
2	2095	99.8	411	9	US-09-828-746-2
3	2095	99.8	411	14	US-10-121-746-83
4	2095	99.8	411	16	US-10-745-210-2
5	2095	99.8	411	16	US-10-349-528-31
6	2095	99.8	411	17	US-10-976-644-83
7	2095	99.8	411	17	US-10-976-647-83
8	2099	99.5	422	16	US-10-349-528-20
9	2062	98.2	426	8	US-08-816-011-45
10	2062	98.2	426	17	US-10-870-492-45
11	2058	98.0	426	17	US-10-870-492-57
Sequence 18, Appl					
Sequence 2, Appl					
Sequence 83, Appl					
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Sequence 31, Appl					
Sequence 83, Appl					
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Sequence 20, Appl					
Sequence 45, Appl					
Sequence 45, Appl					
Sequence 57, Appl					

12	2057	98.0	426	17	US-10-870-492-58	Sequence 58, Appl
13	2054	97.8	426	17	US-10-870-492-60	Sequence 60, Appl
14	2053	97.8	426	17	US-10-870-492-59	Sequence 59, Appl
15	2035	96.9	411	9	US-09-828-746-6	Sequence 6, Appl
16	1824	86.9	370	9	US-09-939-484-8	Sequence 8, Appl
17	1824	86.9	370	9	US-09-939-483-8	Sequence 8, Appl
18	1249	59.5	538	9	US-09-729-920-5	Sequence 5, Appl
19	1249	59.5	538	16	US-10-887-932-5	Sequence 5, Appl
20	1243	59.2	526	16	US-09-729-920-4	Sequence 4, Appl
21	1243	59.2	526	16	US-10-887-932-4	Sequence 4, Appl
22	1243	59.2	538	11	US-09-892-360-2	Sequence 2, Appl
23	1243	59.2	538	18	US-10-923-035-46	Sequence 46, Appl
24	1243	59.2	543	9	US-09-729-920-2	Sequence 2, Appl
25	1243	59.2	543	10	US-09-852-386-73	Sequence 73, Appl
26	1243	59.2	543	14	US-10-332-175-2	Sequence 2, Appl
27	1243	59.2	543	15	US-10-262-511-106	Sequence 106, Appl
28	1243	59.2	543	16	US-10-887-932-2	Sequence 2, Appl
29	1215.5	57.9	724	15	US-10-332-447-10	Sequence 10, Appl
30	803	38.2	392	9	US-09-747-835A-55	Sequence 55, Appl
31	803	38.2	392	15	US-10-312-312-55	Sequence 55, Appl
32	803	38.2	393	14	US-10-243-035-2	Sequence 2, Appl
33	803	38.2	419	9	US-09-828-035-2	Sequence 2, Appl
34	803	38.2	419	14	US-10-345-680-44	Sequence 44, Appl
35	803	38.2	419	14	US-10-146-733-29	Sequence 29, Appl
36	803	38.2	419	15	US-10-352-684A-8	Sequence 8, Appl
37	803	38.2	419	15	US-10-391-399-19	Sequence 19, Appl
38	803	38.2	419	16	US-10-768-158-12	Sequence 12, Appl
39	803	38.2	481	18	US-10-852-707-65	Sequence 65, Appl
40	803	38.2	822	18	US-10-852-707-64	Sequence 64, Appl
41	803	38.2	1314	9	US-09-747-835A-29	Sequence 29, Appl
42	803	38.2	1314	15	US-10-312-312-29	Sequence 29, Appl
43	776.5	37.0	398	11	US-09-892-360-19	Sequence 19, Appl
44	732	34.9	924	18	US-10-852-707-66	Sequence 66, Appl
45	732	34.9	1125	18	US-10-852-707-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-892-360-18
; Sequence 18, Application US/09892360
; Publication No. US20040101833A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LESAGE, FLORIAN
; APPLICANT: ROMERY, GEORGES
; TITLE OF INVENTION: HUMAN TREK2, A STRETCH-AND ARACHIDONIC ACID-SENSITIVE
; TITLE OF INVENTION: K+ CHANNEL ACTIVATED BY INHALATIONAL ANESTHETICS AND
; FILE REFERENCE: RILUZOLE
; FILE REFERENCE: 1256-R-00
; CURRENT APPLICATION NUMBER: US/09/892,360
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 60/214,559
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-892-360-18

Query Match	100.0%	Score 2100;	DB 11;	Length 411;
Best Local Similarity	100.0%	Pred. No. 3.7e-188;		
Matches 411;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTFIFLVVLYLI	60	
Db	1	MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTFIFLVVLYLI	60	
QY	61	GATVFKALEQPHSEISORTTIVIQKTFISQHSVCNSTELDELIQIIVAAINAGIPLGWT	120	

Db 61 GATVFKALEQPEHEISORTTIVIQKTFISQHSVCVNSTELDELIQQIVAAINAGIPLGNT 120
QY 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180
Db 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
QY 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVVFWILVGLAYFAAULSMIGDMLRVIS 300
Db 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVVFWILVGLAYFAAULSMIGDMLRVIS 300
QY 301 KKTKEEVEGFRAHAAEWTANVTAEFKETRRRLSVIEYDKFORATSIKRLKLSAELAGNHQ 360
Db 301 KKTKEEVEGFRAHAAEWTANVTAEFKETRRRLSVIEYDKFORATSIKRLKLSAELAGNHQ 360
QY 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVNGLTTPHCAGEEIAVNIENIK 411
Db 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVNGLTTPHCAGEEIAVNIENIK 411

RESULT 2

US-09-828-746-2
; Sequence 2, Application US/09828746
; Patent No. US20020028485A1
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-2

Query Match 99.8%; Score 2095; DB 9; Length 411;
Best Local Similarity 99.8%; Pred. No. 1.1e-187;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAPDLLDPKSAQAQNSKPLSFSTKPTVLSRVESDITINVMKWTSTIFLVVLYLII 60
Db 1 MAAPDLLDPKSAQAQNSKPLSFSTKPTVLSRVESDITINVMKWTSTIFLVVLYLII 60
QY 61 GATVFKALEQPEHEISORTTIVIQKTFISQHSVCVNSTELDELIQQIVAAINAGIPLGNT 120
Db 61 GATVFKALEQPEHEISORTTIVIQKTFISQHSVCVNSTELDELIQQIVAAINAGIPLGNT 120
QY 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180
Db 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
QY 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVVFWILVGLAYFAAULSMIGDMLRVIS 300
Db 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVVFWILVGLAYFAAULSMIGDMLRVIS 300
QY 301 KKTKEEVEGFRAHAAEWTANVTAEFKETRRRLSVIEYDKFORATSIKRLKLSAELAGNHQ 360

Db 301 KKTKEEVEGFRAHAAEWTANVTAEFKETRRRLSVIEYDKFORATSIKRLKLSAELAGNHQ 360
QY 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVNGLTTPHCAGEEIAVNIENIK 411
Db 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVNGLTTPHCAGEEIAVNIENIK 411

RESULT 3

US-10-121-746-83
; Sequence 83, Application US/10121746
; Publication No. US20030036648A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. US20030036648A1el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/121,746
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: US/09/336,643A
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-121-746-83

Query Match 99.8%; Score 2095; DB 14; Length 411;
Best Local Similarity 99.8%; Pred. No. 1.1e-187;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAAPDLLDPKSAQAQNSKPLSFSTKPTVLSRVESDITINVMKWTSTIFLVVLYLII 60
Db 1 MAAPDLLDPKSAQAQNSKPLSFSTKPTVLSRVESDITINVMKWTSTIFLVVLYLII 60
QY 61 GATVFKALEQPEHEISORTTIVIQKTFISQHSVCVNSTELDELIQQIVAAINAGIPLGNT 120
Db 61 GATVFKALEQPEHEISORTTIVIQKTFISQHSVCVNSTELDELIQQIVAAINAGIPLGNT 120
QY 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180
Db 121 SNOISHWDLGSSFFAGTIVTTIGFNGNISPRTEGGKIFCIIYVALLGIPFLFGLLAGVGQ 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
QY 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVVFWILVGLAYFAAULSMIGDMLRVIS 300
Db 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYFKPVVFWILVGLAYFAAULSMIGDMLRVIS 300
QY 301 KKTKEEVEGFRAHAAEWTANVTAEFKETRRRLSVIEYDKFORATSIKRLKLSAELAGNHQ 360
Db 301 KKTKEEVEGFRAHAAEWTANVTAEFKETRRRLSVIEYDKFORATSIKRLKLSAELAGNHQ 360
QY 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVNGLTTPHCAGEEIAVNIENIK 411
Db 361 ELTPCRRTLSVNHLTNERDVLPLPKTESIYVNGLTTPHCAGEEIAVNIENIK 411

RESULT 4

US-10-745-210-2

```
; Sequence 2, Application US/10745210
; Publication No. US2004014385A1
; GENERAL INFORMATION:
; APPLICANT: TONONI, Giulio
; APPLICANT: CIRELLI, Chiara
; FILE OF INVENTION: ION CHANNELS AS TARGETS FOR SLEEP-RELATED DRUGS
; FILE REFERENCE: 054030-0044
; CURRENT APPLICATION NUMBER: US/10/745,210
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: US 60/436,201
; PRIOR FILING DATE: 2001-12-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-745-210-2

Query Match      99.8%; Score 2095; DB 16; Length 411;
Best Local Similarity 99.8%; Pred. No. 1.1e-187;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
Db 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
QY 61 GATVFKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELQIQIIVAAINAGIIPLGNT 120
Db 61 GATVFKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELQIQIIVAAINAGIIPLGNT 120
QY 121 SNQISHWDLGSSFFAGTAVTTTIGFQNIISPRTEGGKIFCIYIYALLGIPFGFLLAGVGQD 180
Db 121 SNQISHWDLGSSFFAGTAVTTTIGFQNIISPRTEGGKIFCIYIYALLGIPFGFLLAGVGQD 180
QY 181 LGTIFGKGIAKVEDTEIKNVSOTKIRIISTIFILPGCVLFVALPAIIFKHIEGWSALD 240
Db 181 LGTIFGKGIAKVEDTEIKNVSOTKIRIISTIFILPGCVLFVALPAIIFKHIEGWSALD 240
QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300
Db 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLAEAGLNHNQ 360
Db 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLAEAGLNHNQ 360
QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEEIAVNIENIK 411
Db 361 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEEIAVNIENIK 411

RESULT 5
US-10-349-528-31
; Sequence 31, Application US/10349528
; Publication No. US2004025366A1
; GENERAL INFORMATION:
; APPLICANT: RAMANATHAN, Chandra
; APPLICANT: GOPAL, Shuba
; APPLICANT: MINTIER, Gabe
; APPLICANT: FEDER, John
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
; FILE OF INVENTION: USE THEREOF
; FILE REFERENCE: D0210
; CURRENT APPLICATION NUMBER: US/10/349,528
; CURRENT FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; ORGANISM: HOMO SAPIENS
US-10-349-528-31
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Query Match      99.8%; Score 2095; DB 16; Length 411;
Best Local Similarity 99.8%; Pred. No. 1.1e-187;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
Db 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
QY 61 GATVFKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELQIQIIVAAINAGIIPLGNT 120
Db 61 GATVFKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELQIQIIVAAINAGIIPLGNT 120
QY 121 SNQISHWDLGSSFFAGTAVTTTIGFQNIISPRTEGGKIFCIYIYALLGIPFGFLLAGVGQD 180
Db 121 SNQISHWDLGSSFFAGTAVTTTIGFQNIISPRTEGGKIFCIYIYALLGIPFGFLLAGVGQD 180
QY 181 LGTIFGKGIAKVEDTEIKNVSOTKIRIISTIFILPGCVLFVALPAIIFKHIEGWSALD 240
Db 181 LGTIFGKGIAKVEDTEIKNVSOTKIRIISTIFILPGCVLFVALPAIIFKHIEGWSALD 240
QY 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300
Db 241 AIYFVVITLTTIGFGDYVAGGSDIEYDFKPVWFWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLAEAGLNHNQ 360
Db 301 KKTKEVGEFRAHAAEWNTANVTAEFKETRRRLSVEIYDKFORATSIKRKLAEAGLNHNQ 360
QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEEIAVNIENIK 411
Db 361 ELTPCRRTLNVNHLTNERDVLPLPKTESIYLNGLTPHCAGEEIAVNIENIK 411

RESULT 6
US-10-976-644-83
; Sequence 83, Application US/10976644
; Publication No. US20050112662A1
; GENERAL INFORMATION:
; APPLICANT: MILLER, Andrew P.
; APPLICANT: CURRAN, Mark Edward
; APPLICANT: HU, Ping
; APPLICANT: RUTTER, Marc
; APPLICANT: WANG, Jian-Wang
; TITLE OF INVENTION: NOVEL HUMAN POTASSIUM CHANNELS
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/976,644
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US/09/336,643
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
; ORGANISM: H. sapiens
US-10-976-644-83

Query Match      99.8%; Score 2095; DB 17; Length 411;
Best Local Similarity 99.8%; Pred. No. 1.1e-187;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
Db 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKKTSTIFLVVLYLII 60
QY 61 GATVFKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELQIQIIVAAINAGIIPLGNT 120
Db 61 GATVFKALEQPHEISORTTIVIQKQTFISQHSVCNSTELDELQIQIIVAAINAGIIPLGNT 120
```

Db 61 GATVFKALEQPHIEISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120
QY 121 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGLLAGVGQD 180
Db 121 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
QY 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDMLRVIS 300
Db 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDMLRVIS 300
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSIKRKLSAELAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSIKRKLSAELAGNHQ 360
QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 411
Db 361 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 411

RESULT 7

US-10-976-647-83
; Sequence 83, Application US/10976647
; Publication No. US20050112863A1
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: Novel Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/10/976,647
; CURRENT FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: CURRENT APPLICATION NUMBER: US/09/336,643
; PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-976-647-83

Query Match 99.8%; Score 2095; DB 17; Length 411;
Best Local Similarity 99.8%; Pred. No. 1.1e-187;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVSDTTINVMKKTSTIFLVVLYLII 60
Db 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVSDTTINVMKKTSTIFLVVLYLII 60
QY 61 GATVFKALEQPHIEISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120
Db 61 GATVFKALEQPHIEISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120
QY 121 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGLLAGVGQD 180
Db 121 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGLLAGVGQD 180
QY 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240

QY 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDMLRVIS 300
Db 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDMLRVIS 300
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSIKRKLSAELAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSIKRKLSAELAGNHQ 360
QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 411
Db 361 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 411

RESULT 8

US-10-349-528-20
; Sequence 20, Application US/10349528
; Publication No. US20040253668A1
; GENERAL INFORMATION:
; APPLICANT: RAMANATHAN, Chandra
; APPLICANT: GOPAL, Shuba
; APPLICANT: MINTIER, Gabe
; APPLICANT: FEDER, John
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR (GPCR) VARIANTS AND METHODS OF
; FILE REFERENCE: D0210
; CURRENT APPLICATION NUMBER: US/10/349,528
; CURRENT FILING DATE: 2003-01-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 422
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-349-528-20

Query Match 99.5%; Score 2089; DB 16; Length 422;
Best Local Similarity 99.3%; Pred. No. 4.1e-187;
Matches 408; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVSDTTINVMKKTSTIFLVVLYLII 60
Db 12 LAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVSDTTINVMKKTSTIFLVVLYLII 71
QY 61 GATVFKALEQPHIEISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 120
Db 72 GATVFKALEQPHIEISQRTTIVIQKQTFISQHSVCNSTDDELIIQIVAAINAGIPLGNT 131
QY 121 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGLLAGVGQD 180
Db 132 SNQISHWDLGSSFFPAGTVTTTIGFNGISPRTEGGKIFCIIYVALLGIPFGLLAGVGQD 191
QY 181 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 192 LGTIFGKGIKVEDTFIKWNVSQTKIRIISTITIFILFGCVLFVALPAIIFKHIEGWSALD 251
QY 241 AIYFVVTITLTITGFGDYVAGGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDMLRVIS 300
Db 252 AIYFVVTITLTITGFGDYVAGGSDIEYLDYKPVVFWMLVGLAYFAAIVLSMIGDMLRVIS 311
QY 301 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSIKRKLSAELAGNHQ 360
Db 312 KKTKEEVGEFRAHAAEWNTANVTAEFKETRRRLSVIYDKFORATSIKRKLSAELAGNHQ 371
QY 361 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 411
Db 372 ELTPCRRTLNVNHLTNERDVLPLPKTSEIYVNGLTTPHCAGEEIAVIENIK 422

RESULT 9

US-08-816-011-45
; Sequence 45, Application US/08816011
; Publication No. US20030165806A1

Publication No. US20050032165A1
GENERAL INFORMATION:
APPLICANT: PAUSCH, MARK H.
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
TITLE OF INVENTION: AND METHODS OF USING SAME
FILE REFERENCE: 01142.0114 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/10/870,492
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: US/09/503,849
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/816,011
PRIOR FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: PCT/US95/14364
PRIOR FILING DATE: 1995-10-25
PRIOR APPLICATION NUMBER: 07/332,312
PRIOR FILING DATE: 1994-10-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 45
LENGTH: 426
TYPE: PRT
ORGANISM: Homo sapiens
US-10-870-492-45

Query Match 98.2%; Score 2062; DB 17; Length 426;
Best Local Similarity 98.5%; Pred. No. 1.4e-184;
Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPLSSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
DB 16 VAAPDLLDPKSAQNSKPLSSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 75
QY 61 GATVFKALQEPHEISORTTIVIQKQTFISQHSVCNSTELDELIQQIIVAAINAGIIPLGNT 120
DB 76 GATVFKALQEPHEISORTTIVIQKQTFISQHSVCNSTELDELIQQIIVAAINAGIIPLGNT 135
QY 121 SNQISHWDLGSSFFAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFLFGFLLAGVGQD 180
DB 136 SNQISHWDLGSSFFAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFLFGFLLAGVGQD 195
QY 181 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
DB 196 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255
QY 241 AIYFVVITTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDLRVIS 300
DB 256 AIYFVVITTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDLRVIS 315
QY 301 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360
DB 316 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 375
QY 361 ELTPCRTLNVNHLNTERDVLPLLKTESIYNGLTPHCAGEIAVIENIK 411
DB 376 ELTPCRTLNVNHLNTERDVLPLLKTESIYNGLTPHCAGEIAVIENIK 426

RESULT 11
US-10-870-492-57
Sequence 57, Application US/10870492
Publication No. US20050032165A1
GENERAL INFORMATION:
APPLICANT: PAUSCH, MARK H.
TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
TITLE OF INVENTION: AND METHODS OF USING SAME
FILE REFERENCE: 01142.0114 SEQUENCE LISTING
CURRENT APPLICATION NUMBER: US/10/870,492
CURRENT FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: US/09/503,849
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/816,011
PRIOR FILING DATE: 1997-03-11
PRIOR APPLICATION NUMBER: PCT/US95/14364

GENERAL INFORMATION:
APPLICANT: Price, Laura A.
APPLICANT: Pausch, Mark H.
TITLE OF INVENTION: Potassium Channels, Nucleotide Sequences
TITLE OF INVENTION: Encoding Them, and Methods of Using Same
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Home Products Corporation
STREET: One Campus Drive
CITY: Parsippany
STATE: New Jersey
COUNTRY: USA
ZIP: 07054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,011
FILING DATE: 11-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Matthews, Gale F.
REGISTRATION NUMBER: 32,269
REFERENCE/DOCKET NUMBER: 32,421-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-683-2134
TELEFAX: 201-683-4117
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-816-011-45

Query Match 98.2%; Score 2062; DB 8; Length 426;
Best Local Similarity 98.5%; Pred. No. 1.4e-184;
Matches 405; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPLSSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
DB 16 VAAPDLLDPKSAQNSKPLSSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 75
QY 61 GATVFKALQEPHEISORTTIVIQKQTFISQHSVCNSTELDELIQQIIVAAINAGIIPLGNT 120
DB 76 GATVFKALQEPHEISORTTIVIQKQTFISQHSVCNSTELDELIQQIIVAAINAGIIPLGNT 135
QY 121 SNQISHWDLGSSFFAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFLFGFLLAGVGQD 180
DB 136 SNQISHWDLGSSFFAGTVITTTIGFNGISPRTEGGKIFCIIYALLGIPFLFGFLLAGVGQD 195
QY 181 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
DB 196 LGTIFGKIAKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255
QY 241 AIYFVVITTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDLRVIS 300
DB 256 AIYFVVITTTIGFGDYVAGGSDIEYLDYKPVWFWILVGLAYFAAVLSMIGDLRVIS 315
QY 301 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 360
DB 316 KKTKEVGFRAHAAEWTANVTAEFKETRRRLSVEIYDKFORATSIKRKLSAELAGNHQ 375
QY 361 ELTPCRTLNVNHLNTERDVLPLLKTESIYNGLTPHCAGEIAVIENIK 411
DB 376 ELTPCRTLNVNHLNTERDVLPLLKTESIYNGLTPHCAGEIAVIENIK 426

RESULT 10
US-10-870-492-45
Sequence 45, Application US/10870492

		Matches 404; Conservative 4; Mismatches 3; Indels 0; Gaps 0;	
		Query Match 97.8%; Score 2054; DB 17; Length 426;	
		Best Local Similarity 98.3%; Pred. No. 8e-184;	
		Matches 404; Conservative 3; Mismatches 4; Indels 0; Gaps 0;	
QY	1	MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII	60
	16	VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII	75
QY	61	GATVFKALEQPEHSORTTIVIQKTFISQHSVCNVSTELDELIQOIVAAINAGIIPLGNT	120
	76	GATVFKALEQPEHSORTTIVIQKTFISQHSVCNVSTELDELIQOIVAAINAGIIPLGNT	135
QY	121	SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLLAGVGQD	180
	136	SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLLAGVGQD	195
QY	181	LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD	240
	196	LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD	255
QY	241	AIYFVVIITLTITGFGDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDLWRVIS	300
	256	AIYFVVIITLTITGFGDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDLWRVIS	315
QY	301	KKTEEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGNHQ	360
	316	KKTEEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGNHQ	375
QY	361	ELTPCRRTLNVNHLTNERDVLPLPKTESIYVLLGLTPHCAGEEIAVNIENIK	411
	376	ELTPCRRTLNVNHLTNERDVLPLPKTESIYVLLGLTPHCAGEEIAVNIENIK	426
RESULT 13			
US-10-870-492-60			
; Sequence 60, Application US/10870492			
; Publication No. US20050032165A1			
; GENERAL INFORMATION:			
; APPLICANT: PAUSCH, MARK H.			
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,			
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING			
; CURRENT FILING DATE: 2004-06-18			
; PRIOR APPLICATION NUMBER: US/09/503,849			
; PRIOR FILING DATE: 2000-02-15			
; PRIOR APPLICATION NUMBER: 08/816,011			
; PRIOR FILING DATE: 1997-03-11			
; PRIOR APPLICATION NUMBER: PCT/US95/14364			
; PRIOR FILING DATE: 1995-10-25			
; PRIOR APPLICATION NUMBER: 07/332,312			
; PRIOR FILING DATE: 1994-10-31			
; NUMBER OF SEQ ID NOS: 74			
; SOFTWARE: Patent In Ver. 2.1			
; SEQ ID NO 60			
; LENGTH: 426			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-870-492-60			
QY	1	MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII	60
	16	VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII	75
QY	61	GATVFKALEQPEHSORTTIVIQKTFISQHSVCNVSTELDELIQOIVAAINAGIIPLGNT	120
	76	GATVFKALEQPEHSORTTIVIQKTFISQHSVCNVSTELDELIQOIVAAINAGIIPLGNT	135
QY	121	SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLLAGVGQD	180
	136	SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLLAGVGQD	195
QY	181	LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD	240
	196	LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD	255
QY	241	AIYFVVIITLTITGFGDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDLWRVIS	300
	256	TIYFVVIITLTITGFGDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDLWRVIS	315
QY	301	KKTEEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGNHQ	360
	316	KKTEEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGNHQ	375
QY	361	ELTPCRRTLNVNHLTNERDVLPLPKTESIYVLLGLTPHCAGEEIAVNIENIK	411
	376	ELTPCRRTLNVNHLTNERDVLPLPKTESIYVLLGLTPHCAGEEIAVNIENIK	426
RESULT 12			
US-10-870-492-58			
; Sequence 58, Application US/10870492			
; Publication No. US20050032165A1			
; GENERAL INFORMATION:			
; APPLICANT: PAUSCH, MARK H.			
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,			
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING			
; CURRENT FILING DATE: 2004-06-18			
; PRIOR APPLICATION NUMBER: US/09/503,849			
; PRIOR FILING DATE: 2000-02-15			
; PRIOR APPLICATION NUMBER: 08/816,011			
; PRIOR FILING DATE: 1997-03-11			
; PRIOR APPLICATION NUMBER: PCT/US95/14364			
; PRIOR FILING DATE: 1995-10-25			
; PRIOR APPLICATION NUMBER: 07/332,312			
; PRIOR FILING DATE: 1994-10-31			
; NUMBER OF SEQ ID NOS: 74			
; SOFTWARE: Patent In Ver. 2.1			
; SEQ ID NO 58			
; LENGTH: 426			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-870-492-58			
QY	1	MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII	60
	16	VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII	75
QY	61	GATVFKALEQPEHSORTTIVIQKTFISQHSVCNVSTELDELIQOIVAAINAGIIPLGNT	120
	76	GATVFKALEQPEHSORTTIVIQKTFISQHSVCNVSTELDELIQOIVAAINAGIIPLGNT	135
QY	121	SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLLAGVGQD	180
	136	SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLLAGVGQD	195
QY	181	LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD	240
	196	LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD	255
QY	241	AIYFVVIITLTITGFGDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDLWRVIS	300
	256	TIYFVVIITLTITGFGDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDLWRVIS	315
QY	301	KKTEEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGNHQ	360
	316	KKTEEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGNHQ	375
QY	361	ELTPCRRTLNVNHLTNERDVLPLPKTESIYVLLGLTPHCAGEEIAVNIENIK	411
	376	ELTPCRRTLNVNHLTNERDVLPLPKTESIYVLLGLTPHCAGEEIAVNIENIK	426
RESULT 12			
US-10-870-492-58			
; Sequence 58, Application US/10870492			
; Publication No. US20050032165A1			
; GENERAL INFORMATION:			
; APPLICANT: PAUSCH, MARK H.			
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,			
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING			
; CURRENT FILING DATE: 2004-06-18			
; PRIOR APPLICATION NUMBER: US/09/503,849			
; PRIOR FILING DATE: 2000-02-15			
; PRIOR APPLICATION NUMBER: 08/816,011			
; PRIOR FILING DATE: 1997-03-11			
; PRIOR APPLICATION NUMBER: PCT/US95/14364			
; PRIOR FILING DATE: 1995-10-25			
; PRIOR APPLICATION NUMBER: 07/332,312			
; PRIOR FILING DATE: 1994-10-31			
; NUMBER OF SEQ ID NOS: 74			
; SOFTWARE: Patent In Ver. 2.1			
; SEQ ID NO 58			
; LENGTH: 426			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-870-492-58			
QY	1	MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII	60
	16	VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII	75
QY	61	GATVFKALEQPEHSORTTIVIQKTFISQHSVCNVSTELDELIQOIVAAINAGIIPLGNT	120
	76	GATVFKALEQPEHSORTTIVIQKTFISQHSVCNVSTELDELIQOIVAAINAGIIPLGNT	135
QY	121	SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLLAGVGQD	180
	136	SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLLAGVGQD	195
QY	181	LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD	240
	196	LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD	255
QY	241	AIYFVVIITLTITGFGDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDLWRVIS	300
	256	TIYFVVIITLTITGFGDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDLWRVIS	315
QY	301	KKTEEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGNHQ	360
	316	KKTEEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGNHQ	375
QY	361	ELTPCRRTLNVNHLTNERDVLPLPKTESIYVLLGLTPHCAGEEIAVNIENIK	411
	376	ELTPCRRTLNVNHLTNERDVLPLPKTESIYVLLGLTPHCAGEEIAVNIENIK	426
RESULT 12			
US-10-870-492-58			
; Sequence 58, Application US/10870492			
; Publication No. US20050032165A1			
; GENERAL INFORMATION:			
; APPLICANT: PAUSCH, MARK H.			
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,			
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING			
; CURRENT FILING DATE: 2004-06-18			
; PRIOR APPLICATION NUMBER: US/09/503,849			
; PRIOR FILING DATE: 2000-02-15			
; PRIOR APPLICATION NUMBER: 08/816,011			
; PRIOR FILING DATE: 1997-03-11			
; PRIOR APPLICATION NUMBER: PCT/US95/14364			
; PRIOR FILING DATE: 1995-10-25			
; PRIOR APPLICATION NUMBER: 07/332,312			
; PRIOR FILING DATE: 1994-10-31			
; NUMBER OF SEQ ID NOS: 74			
; SOFTWARE: Patent In Ver. 2.1			
; SEQ ID NO 58			
; LENGTH: 426			
; TYPE: PRT			
; ORGANISM: Homo sapiens			
US-10-870-492-58			
QY	1	MAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII	60
	16	VAAPDLLDPKSAQAQNSKPRLSFSTKPTVLASRVESDITINVMKWTSTIFLWVLYLII	75
QY	61	GATVFKALEQPEHSORTTIVIQKTFISQHSVCNVSTELDELIQOIVAAINAGIIPLGNT	120
	76	GATVFKALEQPEHSORTTIVIQKTFISQHSVCNVSTELDELIQOIVAAINAGIIPLGNT	135
QY	121	SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLLAGVGQD	180
	136	SNQISHWDLGSSFFPAGTIVITIGFNGISPRTEGGKIFCIIYVALLGIPFLGFLLAGVGQD	195
QY	181	LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD	240
	196	LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPALIFKHIEGWSALD	255
QY	241	AIYFVVIITLTITGFGDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDLWRVIS	300
	256	TIYFVVIITLTITGFGDYVAGGSDIEYDFYKPVVFWILVGLAYFAAVLSMIGDLWRVIS	315
QY	301	KKTEEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGNHQ	360
	316	KKTEEVGEFRAHAAEWNTANVTAEFKETRRLSVEIYDKFORATSIKRKLSAELAGNHQ	375
QY	361	ELTPCRRTLNVNHLTNERDVLPLPKTESIYVLLGLTPHCAGEEIAVNIENIK	411
	376	ELTPCRRTLNVNHLTNERDVLPLPKTESIYVLLGLTPHCAGEEIAVNIENIK	426
RESULT 12			
US-10-870-492-58			
; Sequence 58, Application US/10870492			
; Publication No. US20050032165A1			
; GENERAL INFORMATION:			
; APPLICANT: PAUSCH, MARK H.			
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,			
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING			
; CURRENT FILING DATE: 2004-06-18			
; PRIOR APPLICATION NUMBER: US/09/503,849			
; PRIOR FILING DATE: 2000-02-15			
; PRIOR APPLICATION NUMBER: 08/816,011			
; PRIOR FILING DATE: 1997-03-11			
; PRIOR APPLICATION NUMBER: PCT/US95/14364			

Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255
Qy 241 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300
Db 256 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDMLRVIS 315
Qy 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRLRSVEIYDKFORATSIKRKLSAELAGNHQ 360
Db 316 KKTKEEVGEFRAHAAEWTANVTAEFKETRRLRSVEIYDKFORATSIKRKLSAELAGNHQ 375
Qy 361 ELTPCRTLSTVNLHNTNRDVLPLLLKTESIYLNGLTPHCGAGEIAVIENIK 411
Db 376 ELTPCRTLSTVNLHNTNRDVLPLLLKTESIYLNGLTPHCGAGEIAVIENIK 426
RESULT 14
US-10-870-492-59
; Sequence 59, Application US/10870492
; Publication No. US20050032165A1
; GENERAL INFORMATION:
; APPLICANT: PAUSCH, MARK H.
; TITLE OF INVENTION: POTASSIUM CHANNELS, NUCLEOTIDE SEQUENCES ENCODING THEM,
; FILE REFERENCE: 01142.0114 SEQUENCE LISTING
; CURRENT APPLICATION NUMBER: US/10/870,492
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/09/503,849
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 08/816,011
; PRIOR FILING DATE: 1997-03-11
; PRIOR APPLICATION NUMBER: PCT/US95/14364
; PRIOR FILING DATE: 1995-10-25
; PRIOR APPLICATION NUMBER: 07/332,312
; PRIOR FILING DATE: 1994-10-31
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 59
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-870-492-59
Query Match 97.8%; Score 2053; DB 17; Length 426;
Best Local Similarity 98.1%; Pred. No. 9.9e-184;
Matches 403; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
Db 16 VAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 75
Qy 61 GATVFKALQEPHEISORTTIVIQOTFISQHSVCNSTELDELIIQOIVAAINAGIIPLGNT 120
Db 76 GATVFKALQEPHEISORTTIVIQOTFISQHSVCNSTELDELIIQOIVAAINAGIIPLGNT 135
Qy 121 SNOISHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
Db 136 SNOISHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 195
Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 196 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 255
Qy 241 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300
Db 256 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDMLRVIS 315
Qy 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRLRSVEIYDKFORATSIKRKLSAELAGNHQ 360
Db 316 KKTKEEVGEFRAHAAEWTANVTAEFKETRRLRSVEIYDKFORATSIKRKLSAELAGNHQ 375

Qy 361 ELTPCRTLSTVNLHNTNRDVLPLLLKTESIYLNGLTPHCGAGEIAVIENIK 411
Db 376 ELTPCRTLSTVNLHNTNRDVLPLLLKTESIYLNGLTPHCGAGEIAVIENIK 426
RESULT 15
US-09-828-746-6
; Sequence 6, Application US/09828746
; Patent No. US20020028485A1
; GENERAL INFORMATION:
; APPLICANT: Helen Jane Meadows
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30031-D1
; CURRENT APPLICATION NUMBER: US/09/828,746
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: US 09/236,080
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: EP 98300570.3
; PRIOR FILING DATE: 1998-01-27
; PRIOR APPLICATION NUMBER: UK 9822135.1
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-746-6
Query Match 96.9%; Score 2035; DB 9; Length 411;
Best Local Similarity 95.9%; Pred. No. 4.6e-182;
Matches 394; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
Db 1 MAAPDLLDPKSAQNSKPRLSFSTKPTVLASRVESDTTINVMKWKTVSTIFLVVLYLII 60
Qy 61 GATVFKALQEPHEISORTTIVIQOTFISQHSVCNSTELDELIIQOIVAAINAGIIPLGNT 120
Db 61 GATVFKALQEPHEISORTTIVIQOTFISQHSVCNSTELDELIIQOIVAAINAGIIPLGNS 120
Qy 121 SNOISHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
Db 121 SNOISHWDLGSSFFPAGTVITTTIGFNIISPRTEGGKIFCIIYALLGIPLFGFLLAGVGDQ 180
Qy 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTIIIFILFGCVLFVALPAIIFKHIEGWSALD 240
Qy 241 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300
Db 241 AIYFVWITLTITIGDYGAGSDIEYLDYFKPVVWFILVGLAYFAAVLSMIGDMLRVIS 300
Qy 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRLRSVEIYDKFORATSIKRKLSAELAGNHQ 360
Db 301 KKTKEEVGEFRAHAAEWTANVTAEFKETRRLRSVEIYDKFORATSIKRKLSAELAGNHQ 360
Qy 361 ELTPCRTLSTVNLHNTNRDVLPLLLKTESIYLNGLTPHCGAGEIAVIENIK 411
Db 361 ELTPCRTLSTVNLHNTNRDVLPLLLKTESIYLNGLTPHCGAGEIAVIENMK 411
Search completed: July 13, 2005, 09:07:00
Job time : 92.2442 secs

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OM protein - protein search, using sw model

Run on: July 13, 2005, 08:10:49 ; Search time 26.3635 Seconds
(without alignments)
1163.760 Million cell updates/sec

Title: US-09-503-089A-2
Perfect score: 2100
Sequence: 1 MAAPDLLDPKSAQNSKPL.....LNLTPHCAGEIAVNIENIK 411

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2095	99.8	411	3	US-09-236-080-2
2	2095	99.8	411	3	US-09-336-643A-83
3	2035	96.9	411	3	US-09-236-080-6
4	1824	86.9	370	3	US-09-144-914-8
5	1243	59.2	538	4	US-09-949-016-7001
6	1243	59.2	558	4	US-09-949-016-7368
7	803	38.2	393	4	US-09-432-470-2
8	803	38.2	393	4	US-09-432-470-4
9	803	38.2	419	4	US-09-949-016-6913
10	803	38.2	440	4	US-09-949-016-7809
11	547	26.0	107	3	US-09-236-080-4
12	427	20.3	499	4	US-09-561-763-2
13	427	20.3	499	4	US-09-431-367B-2
14	391	18.6	332	4	US-09-561-763-5
15	391	18.6	332	4	US-09-431-367B-5
16	382	18.2	361	4	US-09-362-842-14
17	379.5	18.1	336	3	US-08-749-816-2
18	379.5	18.1	336	3	US-09-144-914-2
19	363	17.3	394	3	US-09-144-914-4
20	349.5	16.6	388	4	US-09-949-016-7631
21	348	16.6	313	3	US-09-336-643A-81
22	348	16.6	313	4	US-09-561-763-8
23	348	16.6	313	4	US-09-431-367B-8
24	337	16.0	405	3	US-09-144-914-5
25	309.5	14.7	408	4	US-09-362-842-12
26	291.5	13.9	618	1	US-08-332-312-2
27	284	13.5	257	4	US-09-949-016-6654

28	284	13.5	273	4	US-09-949-016-7794	Sequence 7794, Ap
29	261.5	12.5	395	4	US-09-362-842-6	Sequence 6, Appli
30	221.5	10.5	730	4	US-09-362-842-4	Sequence 4, Appli
31	221.5	10.5	741	4	US-09-362-842-67	Sequence 67, Appli
32	221.5	10.5	741	4	US-09-270-767-45442	Sequence 45442, A
33	221	10.5	336	1	US-08-332-312-4	Sequence 4, Appli
34	209	10.0	995	4	US-09-362-842-2	Sequence 2, Appli
35	205	9.8	401	4	US-09-561-763-11	Sequence 11, Appli
36	205	9.8	401	4	US-09-431-367B-11	Sequence 11, Appli
37	179	8.5	383	3	US-08-749-816-4	Sequence 4, Appli
38	179	8.5	383	3	US-09-144-914-7	Sequence 7, Appli
39	166.5	7.9	1153	4	US-09-362-842-8	Sequence 8, Appli
40	160.5	7.6	347	3	US-08-749-816-3	Sequence 3, Appli
41	160.5	7.6	347	3	US-09-144-914-6	Sequence 6, Appli
42	153.5	7.3	197	3	US-09-336-643A-16	Sequence 16, Appli
43	140	6.7	146	4	US-09-362-842-69	Sequence 69, Appli
44	140	6.7	146	4	US-09-270-767-31685	Sequence 31685, A
45	130.5	6.2	391	4	US-09-543-681A-7029	Sequence 7029, Ap

ALIGNMENTS

RESULT 1
US-09-236-080-2
; Sequence 2, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-2

Query Match	99.8%	Score	2095;	DB	3;	Length	411;
Best Local Similarity	99.8%	Pred. No.	4.7e-205;				
Matches	410;	Conservative	1;	Mismatches	0;	Indels	0;
						Gaps	0;
QY	1	MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKKTSTFIWVVLII	60				
Db	1	MAAPDLLDPKSAQNSKPLSPSTKPTVLASRVESDTTINVMKKTSTFIWVVLII	60				
QY	61	GATVFKALEQPEHEISQRTTIVIQKTFISQHSVSNSTELDELIQQIVAAINAGIPLGNT	120				
Db	61	GATVFKALEQPEHEISQRTTIVIQKTFISQHSVSNSTELDELIQQIVAAINAGIPLGNT	120				
QY	121	SNQISHWDLGSSFFPAGTVITIGFNGISPRTEGGKIFCIIYALLGIPFGLLAGVQDQ	180				
Db	121	SNQISHWDLGSSFFPAGTVITIGFNGISPRTEGGKIFCIIYALLGIPFGLLAGVQDQ	180				
QY	181	LGTIFGKGIKAVDETFIKWNVSQTKIRIISTIFILFGCVLFVALPAIFKHIEGWSALD	240				
Db	181	LGTIFGKGIKAVDETFIKWNVSQTKIRIISTIFILFGCVLFVALPAIFKHIEGWSALD	240				
QY	241	AIYFVVIITLTITGFDYVAGSDIEYLFQKPVWFWILVGLAYFAAULSMIGDMLRVIS	300				
Db	241	AIYFVVIITLTITGFDYVAGSDIEYLFQKPVWFWILVGLAYFAAULSMIGDMLRVIS	300				
QY	301	KKTKEVGEFRAHAAEWNTANVTAEPKTRRLRSVEIYDKFORATSIKRLKSLAELAGNHQ	360				
Db	301	KKTKEVGEFRAHAAEWNTANVTAEPKTRRLRSVEIYDKFORATSIKRLKSLAELAGNHQ	360				
QY	361	ELTPCRRLTSVNHLTNRDVLPLKTSIYINGLTTPHCAGEIAVNIENIK	411				
Db	361	ELTPCRRLTSVNHLTNRDVLPLKTSIYINGLTTPHCAGEIAVNIENIK	411				

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RESULT 2
US-09-336-643A-83
; Sequence 83, Application US/09336643A
; Patent No. 6399761
; GENERAL INFORMATION:
; APPLICANT: Miller, Andrew P.
; APPLICANT: Curran, Mark Edward
; APPLICANT: Hu, Ping
; APPLICANT: Rutter, Marc
; APPLICANT: Wang, Jian-Wang
; TITLE OF INVENTION: No. 6399761el Human Potassium Channels
; FILE REFERENCE: SEQ-15P
; CURRENT APPLICATION NUMBER: US/09/336,643A
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 60/076,687
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: 60/116,448
; PRIOR FILING DATE: 1999-01-19
; PRIOR APPLICATION NUMBER: PCT/US99/03826
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 411
; TYPE: PRT
; ORGANISM: H. sapiens
US-09-336-643A-83

Query Match          99.8%; Score 2095; DB 3; Length 411;
Best Local Similarity 99.8%; Pred. No. 4.7e-205;
Matches 410; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVSDTTINNMKKTSTFIPLVVLYLI 60
Db 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVSDTTINNMKKTSTFIPLVVLYLI 60
QY 61 GATVFKALEQPEHEISQRTTIVIQKTFISQHSVCNSTDDELIOQIVAAINAGIPLGNT 120
Db 61 GATVFKALEQPEHEISQRTTIVIQKTFISQHSVCNSTDDELIOQIVAAINAGIPLGNT 120
QY 121 SNOISHWDLGSSFFAGTIVITIGFNIISPRTEGGKIFCIIYALLGIPFGFLLAGVG 180
Db 121 SNOISHWDLGSSFFAGTIVITIGFNIISPRTEGGKIFCIIYALLGIPFGFLLAGVG 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAIFKHIEGWSALD 240
QY 241 AIYFVVTITLTGFGDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300
Db 241 AIYFVVTITLTGFGDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAHAAEWNTANTAEFKETRRLSVIYDKFORATSIKRLSIAELAGNHQ 360
Db 301 KKTKEVGEFRAHAAEWNTANTAEFKETRRLSVIYDKFORATSIKRLSIAELAGNHQ 360
QY 361 ELTPCRRRLTSVNHLTNRDVLPLLKTESIYLNGLTPHCAGEIAVIENIK 411
Db 361 ELTPCRRRLTSVNHLTNRDVLPLLKTESIYLNGLTPHCAGEIAVIENIK 411

RESULT 3
US-09-236-080-6
; Sequence 6, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080

Query Match          86.9%; Score 1824; DB 3; Length 370;
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; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-236-080-6

Query Match          96.9%; Score 2035; DB 3; Length 411;
Best Local Similarity 95.9%; Pred. No. 6.2e-199;
Matches 394; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVSDTTINNMKKTSTFIPLVVLYLI 60
Db 1 MAAPDLLDPKSAQNSKPLSFSTKPTVLASRVSDTTINNMKKTSTFIPLVVLYLI 60
QY 61 GATVFKALEQPEHEISQRTTIVIQKTFISQHSVCNSTDDELIOQIVAAINAGIPLGNT 120
Db 61 GATVFKALEQPEHEISQRTTIVIQKTFISQHSVCNSTDDELIOQIVAAINAGIPLGNT 120
QY 121 SNOISHWDLGSSFFAGTIVITIGFNIISPRTEGGKIFCIIYALLGIPFGFLLAGVG 180
Db 121 SNOISHWDLGSSFFAGTIVITIGFNIISPRTEGGKIFCIIYALLGIPFGFLLAGVG 180
QY 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAIFKHIEGWSALD 240
Db 181 LGTIFGKGIKVEDTFIKWNSQTKIRIISTITIFLFGCVLFVALPAIFKHIEGWSALD 240
QY 241 AIYFVVTITLTGFGDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300
Db 241 AIYFVVTITLTGFGDYVAGGSDIEYLDYKPVVWFWILVGLAYFAAVLSMIGDMLRVIS 300
QY 301 KKTKEVGEFRAHAAEWNTANTAEFKETRRLSVIYDKFORATSIKRLSIAELAGNHQ 360
Db 301 KKTKEVGEFRAHAAEWNTANTAEFKETRRLSVIYDKFORATSIKRLSIAELAGNHQ 360
QY 361 ELTPCRRRLTSVNHLTNRDVLPLLKTESIYLNGLTPHCAGEIAVIENIK 411
Db 361 ELTPCRRRLTSVNHLTNRDVLPLLKTESIYLNGLTPHCAGEIAVIENIK 411

RESULT 4
US-09-144-914-8
; Sequence 8, Application US/09144914
; Patent No. 6309855
; GENERAL INFORMATION:
; APPLICANT: Duprat, Fabrice
; APPLICANT: Lesage, Florian
; APPLICANT: Pink, Michel
; APPLICANT: Lazdunski, Michel
; TITLE OF INVENTION: FAMILY OF MAMMALIAN POTASSIUM CHANNELS, THEIR CLONING
; TITLE OF INVENTION: AND THEIR USE, ESPECIALLY FOR THE SCREENING OF DRUGS
; FILE REFERENCE: 989.6705CIP
; CURRENT APPLICATION NUMBER: US/09/144,914
; CURRENT FILING DATE: 1998-09-01
; EARLIER APPLICATION NUMBER: 08/749,816
; EARLIER FILING DATE: 1996-11-15
; EARLIER APPLICATION NUMBER: 60/095,234
; EARLIER FILING DATE: 1998-08-04
; EARLIER APPLICATION NUMBER: FR 96/01565
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Murine
; FEATURE:
; OTHER INFORMATION: TREK-1
US-09-144-914-8

Query Match          86.9%; Score 1824; DB 3; Length 370;
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Best Local Similarity 96.5%; Pred. No. 1.8e-177;
Matches 355; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAAPDLLDPKSAQNSKPRLSFTKPTVLASRVESDTTNNMKNKTVSTIFLVVLYLII 60
DB 1 MAAPDLLDPKSAQNSKPRLSFTKPTVLASRVESDTTNNMKNKTVSTIFLVVLYLII 60

QY 61 GATVFKALEQPEHISQRTTIVIQKTFISQHSVCNSTELDELIIQIIVAAINAGIIPLGNT 120
DB 61 GAAVFKALEQPEHISQRTTIVIQKTFIAQHACVNSTELDELIIQIIVAAINAGIIPLGNS 120

QY 121 SNOISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPILFGLAGVQDQ 180
DB 121 SNOVSHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPILFGLAGVQDQ 180

QY 181 LGTIFGKGIAKVEDTIFKNVVSQTKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240
DB 181 LGTIFGKGIAKVEDTIFKNVVSQTKIRIISTIFILFGCVLFVALPAIIFKHIEGWSALD 240

QY 241 AIYFVVITLTTIGFDYVAGGSDIEYLDYKPVVWFWLVLGLAYFAAVLSMIGDMLRVIS 300
DB 241 AIYFVVITLTTIGFDYVAGGSDIEYLDYKPVVWFWLVLGLAYFAAVLSMIGDMLRVIS 300

QY 301 KKTKEVGFRAHAAEWNTAETAEFKETRRLRSVEIYDKFORATSIRKLSAELAGNHQ 360
DB 301 KKTKEVGFRAHAAEWNTAETAEFKETRRLRSVEIYDKFORATSIRKLSAELAGNHQ 360

QY 361 ELTPCRR 368
DB 361 ELTPCRR 368

RESULT 5

US-09-949-016-7001
; Sequence 7001, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7001
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7001

Query Match 59.2%; Score 1243; DB 4; Length 538;
Best Local Similarity 62.7%; Pred. No. 6.1e-118;
Matches 247; Conservative 54; Mismatches 65; Indels 28; Gaps 6;

QY 2 AAPDLLDPKSA-----AONSKPRLSFTKPTVLASRVESDT---TNNMKNKTVSTI 50
DB 17 AAAPVQPKSATNGOPPAPPTPTPLRSSRATVVA-RMEGTSGGLQTVNMKKTVAI 75

QY 51 FLVVVLYLIGATVFKALEQPEHISQRTTIVIQKTFISQHSVCNSTELDELIIQIIVAAI 110
DB 76 FVVVVVLYTGLVFRALQPESSQKNTIALEKAEFLRDHVCVSPQELTIQHALDAD 135

QY 111 NAGIPLGNTSNQISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPILF 170
DB 136 NAGVSPIGNSSNNSHWDLGSAFFAGTIVTTIGYGNIAPESTEGGKIFCIIYALFIPILF 195

QY 171 GFLLAGVGDLGTIFGKGIAKVEDTIFKNVVSQTKIRIISTIFILFGCVLFVALPAIIF 230
DB 196 GFLLAGIGDLGTIFGKSIARVEKVPKQVSTQTKIRIVISTILFILAGCIVFTIPAVIF 255

QY 231 KHIEGWSALDAIYFVVITLTTIGFDYVAGG-SDIEYLDYKPVVWFWLVLGLAYFAAVL 289
DB 256 KYIEGWTALESIYFVVVTLTTVGFDFVAGGNAGINREWKYPLVWFWLVLGLAYFAAVL 315

QY 290 SMIGDMLRVISKKTKEVGFRAHAAEWNTAETAEFKETRRLRSVEIYDKFORATSIRK 349
DB 316 SMIGDMLRVLSKKTKEVGEIKAHAAEWKANTAEFRTRRLRSVEIHDKLRQAATIR-- 373

QY 350 LSAELAGNHQBELTPCRRLTSVNNHLTNERDVLPP 383
DB 374 -SME-----RRRLGLDQRAHSLDMLSP 394

RESULT 6
US-09-949-016-7368
; Sequence 7368, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7368
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7368

Query Match 59.2%; Score 1243; DB 4; Length 558;
Best Local Similarity 62.7%; Pred. No. 6.4e-118;
Matches 247; Conservative 54; Mismatches 65; Indels 28; Gaps 6;

QY 2 AAPDLLDPKSA-----AONSKPRLSFTKPTVLASRVESDT---TNNMKNKTVSTI 50
DB 37 AAAPVQPKSATNGOPPAPPTPTPLRSSRATVVA-RMEGTSGGLQTVNMKKTVAI 95

QY 51 FLVVVLYLIGATVFKALEQPEHISQRTTIVIQKTFISQHSVCNSTELDELIIQIIVAAI 110
DB 96 FVVVVVLYTGLVFRALQPESSQKNTIALEKAEFLRDHVCVSPQELTIQHALDAD 155

QY 111 NAGIPLGNTSNQISHWDLGSSFFPAGTIVTTIGFNGISPRTEGGKIFCIIYALLGIPILF 170
DB 156 NAGVSPIGNSSNNSHWDLGSAFFAGTIVTTIGYGNIAPESTEGGKIFCIIYALFIPILF 215

QY 171 GFLLAGVGDLGTIFGKGIAKVEDTIFKNVVSQTKIRIISTIFILFGCVLFVALPAIIF 230
DB 216 GFLLAGIGDLGTIFGKSIARVEKVPKQVSTQTKIRIVISTILFILAGCIVFTIPAVIF 275

QY 231 KHIEGWSALDAIYFVVITLTTIGFDYVAGG-SDIEYLDYKPVVWFWLVLGLAYFAAVL 289
DB 276 KYIEGWTALESIYFVVVTLTTVGFDFVAGGNAGINREWKYPLVWFWLVLGLAYFAAVL 335

QY 290 SMIGDMLRVISKKTKEVGFRAHAAEWNTAETAEFKETRRLRSVEIYDKFORATSIRK 349
DB 336 SMIGDMLRVLSKKTKEVGEIKAHAAEWKANTAEFRTRRLRSVEIHDKLRQAATIR-- 393

QY 350 LSAELAGNHQBELTPCRRLTSVNNHLTNERDVLPP 383
DB 394 -SME-----RRRLGLDQRAHSLDMLSP 414

RESULT 7
US-09-432-470-2
; Sequence 2, Application US/09432470
; Patent No. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; EARLIER FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 393
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-432-470-2

Query Match 38.2%; Score 803; DB 4; Length 393;
Best Local Similarity 51.1%; Pred. No. 3e-73; Mismatches 61; Indels 2; Gaps 1;
Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
QY 42 MKWKTSTIFLVVLYLIIGATVFKALQEPHEISORTTIVIOKQTFISQHSVCNSELDE 101
Db 1 MRSTTLALLALVLYVSGALVFRALEQHPHQQAQRELGEVREKFLRAHPCVSDQELGL 60
QY 102 LIQIIVAANAGIPLGNTSNQISH--WDLGSSPFFAGTIVITIGFNSIPRTEGKIFC 159
Db 61 LIKEVADALGGADPETNSTSSHSAMDLSGSAFFPSGTIIITIGYVVALRTDAGRLFC 120
QY 160 IYVALLGIPFLGAGVDQGTIFGKIAKVEDTFIKWVVSQTKIRIISTIIIFILFC 219
Db 121 IFYALVGIPFLGILLAGVDRGLSGSLRHGIEHIAFLKWHVPPPELVRLVLSAMFLLLGC 180
QY 220 VLFVALPAIIFKHIEGWSALDAIYFVITLTITIGFDYVAGSDIEYLDIFYKPVVWFIL 279
Db 181 LLFVLTPTTFVCYMEDWSKLEAIYFVITLTITIGFDYVAGSDIEYLDIFYKPVVWFIL 240
QY 280 VGLAYFAAVLSMIGDMLRVISKTKKEVGEFRAHAAEWNTAVTA 323
Db 241 LGLAYFASVLTITIGNWLRVSRRTAEMGGLTAQAASWTGTVTA 284

RESULT 8
US-09-432-470-4
; Sequence 4, Application US/09432470
; Patent No. 6426197
; GENERAL INFORMATION:
; APPLICANT: David Malcolm Duckworth
; APPLICANT: Conrad Gerald Chapman
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30190
; CURRENT APPLICATION NUMBER: US/09/432,470
; EARLIER FILING DATE: 1999-11-03
; EARLIER APPLICATION NUMBER: UK 9923668.9
; EARLIER FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: UK 9824048.4
; EARLIER FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 393
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-432-470-4

Query Match 38.2%; Score 803; DB 4; Length 393;
Best Local Similarity 51.1%; Pred. No. 3e-73; Mismatches 61; Indels 2; Gaps 1;
Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
QY 42 MKWKTSTIFLVVLYLIIGATVFKALQEPHEISORTTIVIOKQTFISQHSVCNSELDE 101
Db 1 MRSTTLALLALVLYVSGALVFRALEQHPHQQAQRELGEVREKFLRAHPCVSDQELGL 60
QY 102 LIQIIVAANAGIPLGNTSNQISH--WDLGSSPFFAGTIVITIGFNSIPRTEGKIFC 159
Db 61 LIKEVADALGGADPETNSTSSHSAMDLSGSAFFPSGTIIITIGYVVALRTDAGRLFC 120
QY 160 IYVALLGIPFLGAGVDQGTIFGKIAKVEDTFIKWVVSQTKIRIISTIIIFILFC 219
Db 121 IFYALVGIPFLGILLAGVDRGLSGSLRHGIEHIAFLKWHVPPPELVRLVLSAMFLLLGC 180
QY 220 VLFVALPAIIFKHIEGWSALDAIYFVITLTITIGFDYVAGSDIEYLDIFYKPVVWFIL 279
Db 181 LLFVLTPTTFVCYMEDWSKLEAIYFVITLTITIGFDYVAGSDIEYLDIFYKPVVWFIL 240
QY 280 VGLAYFAAVLSMIGDMLRVISKTKKEVGEFRAHAAEWNTAVTA 323
Db 241 LGLAYFASVLTITIGNWLRVSRRTAEMGGLTAQAASWTGTVTA 284

RESULT 9
US-09-949-016-6913
; Sequence 6913, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6913
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6913

Query Match 38.2%; Score 803; DB 4; Length 419;
Best Local Similarity 51.1%; Pred. No. 3.3e-73; Mismatches 61; Indels 2; Gaps 1;
Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
QY 42 MKWKTSTIFLVVLYLIIGATVFKALQEPHEISORTTIVIOKQTFISQHSVCNSELDE 101
Db 27 MRSTTLALLALVLYVSGALVFRALEQHPHQQAQRELGEVREKFLRAHPCVSDQELGL 86
QY 102 LIQIIVAANAGIPLGNTSNQISH--WDLGSSPFFAGTIVITIGFNSIPRTEGKIFC 159
Db 87 LIKEVADALGGADPETNSTSSHSAMDLSGSAFFPSGTIIITIGYVVALRTDAGRLFC 146
QY 160 IYVALLGIPFLGAGVDQGTIFGKIAKVEDTFIKWVVSQTKIRIISTIIIFILFC 219
Db 147 IFYALVGIPFLGILLAGVDRGLSGSLRHGIEHIAFLKWHVPPPELVRLVLSAMFLLLGC 206
QY 220 VLFVALPAIIFKHIEGWSALDAIYFVITLTITIGFDYVAGSDIEYLDIFYKPVVWFIL 279
Db 207 LLFVLTPTTFVCYMEDWSKLEAIYFVITLTITIGFDYVAGSDIEYLDIFYKPVVWFIL 266
QY 280 VGLAYFAAVLSMIGDMLRVISKTKKEVGEFRAHAAEWNTAVTA 323
Db 267 LGLAYFASVLTITIGNWLRVSRRTAEMGGLTAQAASWTGTVTA 310

RESULT 10
US-09-949-016-7809
; Sequence 7809, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7809
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7809

Query Match 38.2%; Score 803; DB 4; Length 440;
Best Local Similarity 51.1%; Pred. No. 3.5e-73;
Matches 145; Conservative 61; Mismatches 76; Indels 2; Gaps 1;
QY 42 MKWKTSTPLVVLVLIIGATVFKALQEPHEISQRTTIVIQKTFISQHSVCNVTSLDE 101
DB 48 MRSTLLALLALLVLSGALVFRALQEPHEQQAQRELGVREKFLRAHPCVSDQELGL 107
QY 102 LIQOIVAINAGIPLGNTSNQISH--WDLGSSFFPAGTIVITIGFNGNISPRTEGKIFC 159
DB 108 LIKEVADALGGGADPTNSTSSHSANDLGSAPFFSGTIITIGYGNVALRTDAGRLFC 167
QY 160 IYVALLGIFLPGFLAGVGDQLTIFGKGIKVEDTFIKWVNSQTKIRIISTITIFLFGC 219
DB 168 IFYALVGIPLFGILLAGVDRIGSSLRHGIGHIEAIFLKNHVPPELVRLVLSAMFLILGC 227
QY 220 VLFVALPAIIFKHIEGWSALDAIYFVITLTITIGFDGYVAGSDIEYLDYKPVVWFIL 279
DB 228 LLFVLPTTFVFCMEDWSKLEAIYFVITLTITIGFDGYVAGADPRQDSPAYQPLVWFIL 287
QY 280 VGLAYPAAVLSMGDWLRVLSKTKKEVEGEFRAHAAEWNTANVTA 323
DB 288 LGLAYPASVLTITIGNWLRVVSRRTRAEMGGLTAQAASWTGTVTA 331

RESULT 11
US-09-236-080-4
; Sequence 4, Application US/09236080
; Patent No. 6242217
; GENERAL INFORMATION:
; APPLICANT: Helen Meadows
; APPLICANT: Conrad Chapman
; TITLE OF INVENTION: No. 6242217el Compounds
; FILE REFERENCE: GP30031
; CURRENT APPLICATION NUMBER: US/09/236,080
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-236-080-4

Query Match 26.0%; Score 547; DB 3; Length 107;
Best Local Similarity 98.1%; Pred. No. 5.6e-48;

Matches 105; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 119 NTSNQISHWDLGSSFFPAGTIVITIGFNGNISPRTEGKIFCIIYALLGIFLPGFLAGVG 178
DB 1 NSSNQVSHWDLGSSFFPAGTIVITIGFNGNISPRTEGKIFCIIYALLGIFLPGFLAGVG 60
QY 179 DQLTIFGKGIKVEDTFIKWVNSQTKIRIISTITIFLFGCVLFAV 225
DB 61 DQLTIFGKGIKVEDTFIKWVNSQTKIRIISTITIFLFGCVLFAV 107
RESULT 12
US-09-561-763-2
; Sequence 2, Application US/09561763
; Patent No. 6664373
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A. J. et al.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP2
; CURRENT APPLICATION NUMBER: US/09/561,763
; CURRENT FILING DATE: 2000-04-29
; PRIOR APPLICATION NUMBER: 09/431,367
; PRIOR FILING DATE: 01-11-1999
; PRIOR APPLICATION NUMBER: US 09/259,951
; PRIOR FILING DATE: 01-03-1999
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-561-763-2

Query Match 20.3%; Score 427; DB 4; Length 499;
Best Local Similarity 31.1%; Pred. No. 1e-34;
Matches 106; Conservative 60; Mismatches 121; Indels 54; Gaps 11;
QY 54 VVLYLIIGATVFKALQEPHEISQRTTIVIQKTFISQHSVCNVTSLDELIQQIVAAINAG 113
DB 12 IIFLYAIGAIAIPEVLEEPHWEAKKNYYTKLHLLKEPCLGQEGLDKILEVVSDAAGQ 71
QY 114 IPLGNTSNQISHWDLGSSFFPAGTIVITIGFNGNISPRTEGKIFCIIYALLGIFLPGFL 173
DB 72 VAITGNQT--FNNWNPAMIFAATVITIGYGNVAPKTPAGRLFCVYGLGVPPL---C 126
QY 174 LAGVGDQLTIFGKGIKVEDTFIKWVNSQTKIRIISTITIFLFGCVLFAVPAIIFKHI 233
DB 127 LTWII-SALGKPFGRKRLGQPLTKRGVSLRKAQITCTVIFVWGLVHLVIPPFFVMT 185
QY 234 EGWSALDAIYFVITLTITIGFDGYVAG-GSDIEYLDYKPVVWFILVGLAYFAAVLSMI 292
DB 186 EGMNIEGLIYYSFIIITIGFDGVAGVNPNSANYHALYRYFVELMIYLGAW---LSLF 241
QY 293 GDWLRVLSKTKKEVEGEFRAHAAEWNTANVTAEFKTRRLSVEIYDKFORATSIKRLSA 352
DB 242 VNW-----KVSME-----VEVHKAIKRRRR-----RKESF 267
QY 353 ELAGNHNQELTPCRETLSVNHLTNERDV--LPPLKTSIY 391
DB 268 E-SSPHS-----RKALQVKGSTASKVDNIFSLSKKEETY 301

RESULT 13
US-09-431-367B-2
; Sequence 2, Application US/09431367B
; Patent No. 6670149
; GENERAL INFORMATION:
; APPLICANT: Curtis, Roy A. J.
; TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
; FILE REFERENCE: MNI-074CP
; CURRENT APPLICATION NUMBER: US/09/431,367B
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/259,951

